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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:35:08 ; Search time 154 Seconds
(without alignments)
805.976 Million cell updates/sec

Title: us-09-980-049-1

Perfect score: 1788
Sequence: 1 MERKFSLOPSTISVSEMEPN.....KATKCVFVSWLRKTRV 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1788	100.0	346	4 AAB73097	Aab73097 Human LTC
2	1788	100.0	346	4 AAE07538	Aae07538 Human G-P
3	1788	100.0	346	4 AAU07294	Aau07294 Cyte1ny1
4	1788	100.0	346	4 AAB82852	Aab82852 Human P2Y
5	1788	100.0	346	4 AAU04368	Aau04368 Human G-P
6	1788	100.0	346	4 AAE12022	Aae12022 Human G-P
7	1788	100.0	346	5 AAE17231	Aae17231 Human Cys
8	1788	100.0	346	5 AAG77965	Aag77965 Human G-P
9	1788	100.0	346	5 ABP95624	Abp95624 Human GPC
10	1788	100.0	346	5 ABG66884	Abg66884 Human nov
11	1788	100.0	346	5 ABB05229	Abb05229 Human LTD
12	1788	100.0	346	5 AAU10004	Aau10004 Human Cys
13	1788	100.0	346	6 ABU11923	Abu11923 Human G-P
14	1788	100.0	346	6 ABP81707	Abp81707 Human Cys
15	1788	100.0	346	7 ADH00945	Adh00945 Human Cys
16	1788	100.0	346	7 ADL96460	Adl96460 Human G-P
17	1788	100.0	346	7 ADK51004	Adk51004 Human NOV
18	1788	100.0	346	7 ADK51002	Adk51002 Human NOV
19	1788	100.0	346	8 ADG25220	Adg25220 Human Cys
20	1788	100.0	346	8 ADH41891	Adh41891 Novel hum
21	1788	100.0	346	8 ADH41889	Adh41889 Novel hum
22	1788	100.0	346	8 ADO29277	Ado29277 Human GPC
23	1784	99.8	346	8 ADG25233	Adg25233 Human Cys
24	1782	99.7	346	4 AAU04383	Aau04383 Human G-P
25	1782	99.7	346	7 ADL96534	Adl96534 Human mut

26	1779	99.5	346	4 AAE08553	Aae08553 Human G-P
27	1762	98.5	341	4 AAE07539	Aae07539 Human G-P
28	1762	98.5	341	6 ABU11939	Abu11939 Human G-P
29	1749.5	97.8	347	4 AAB85094	Aab85094 Human Cys
30	1712	95.7	330	5 AAG77964	Aag77964 Human G-P
31	1712	95.7	330	6 ABU11900	Abu11900 Human G-P
32	1673.5	93.6	331	4 AAB85097	Aab85097 Truncated
33	1590	88.9	308	6 ABU11962	Abu11962 Human HGP
34	1516	84.8	293	6 ABU11963	Abu11963 Human HGP
35	1427.5	79.8	345	4 AAB73098	Aab73098 Pig LTC4
36	1197	66.9	309	8 ADO29278	Ado29278 Mouse GPC
37	1187	66.4	309	4 AAB73099	Aab73099 Rat LTC4
38	1187	66.4	309	4 AAB85095	Aab85095 Rat CYBLT
39	612	34.2	126	4 AAM25841	Aam25841 Human pro
40	560	31.3	352	8 ADO29276	Ado29276 Mouse GPC
41	559	31.3	337	2 AAW75799	Aaw75799 Human 7-L
42	559	31.3	337	2 AAM85047	Aam85047 A human 7
43	559	31.3	337	4 AAE02492	Aae02492 Human CON
44	559	31.3	337	4 AAB85096	Aab85096 Human Cys
45	559	31.3	337	6 ABU11904	Abu11904 Human Cys

ALIGNMENTS

RESULT 1
AAB73097 standard; protein; 346 AA.
ID AAB73097
AC AAB73097;
XX
XX
DT 05-JUN-2001 (first entry)
XX
XX DE Human LTC4 receptor SEQ ID NO: 2.
XX
XX DE Human LTC4 receptor receptor; LTC4; allergy;
XX
XX KM Human; peptide leukotriene receptor; LTC4; allergy;
XX
XX KM inflammatory disorder.
XX
XX OS Homo sapiens.
XX
XX OS
XX PN WO200119986-A1.
XX
XX PD 22-MAR-2001.
XX
XX PF 13-SEP-2000; 2000WO-JP06265.
XX
XX PR 14-SEP-1999; 99JP-00259986.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX PI Takasaki J, Kamohara M, Matsumoto M, Saito T, Sugimoto T, Oka T;
XX
XX PI Iogaki T, Nishikawa T, Kawai Y;
XX
XX DR WPI; 2001-244800/25.
XX
XX DR N-PSDB; AAF81528.
XX
XX PT New leukotriene C4 receptor protein for screening modifiers of ligand
XX
XX PT binding activity for treating allergic and inflammatory disorders, such
XX
XX PT as ulcerative colitis and asthma.
XX
XX PS Claim 1; Page 63-64; 83pp; Japanese.
XX
XX CC The present invention provides the protein and coding sequences of a
XX
XX CC novel human, pig and rat leukotriene C4 receptor. These sequences can be
XX
XX CC used to screen for substances that can be used in the treatment and
XX
XX CC prevention of allergic and inflammatory disorders including dermatitis,
XX
XX CC inflammatory bowel disease, ulcerative colitis, asthma and bronchitis.
XX
XX CC The present sequence is the human LTC4 receptor
XX
XX SQ Sequence 346 AA;
XX
XX Query Match 100.0%; Score 1788; DB 4; Length 346;

Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MERKMSLOPSISVSEMEBNGTFSNNRNCTIENFKRBPPIVYLIIFFWGLANGLSI 60
DB 1 MERKMSLOPSISVSEMEBNGTFSNNRNCTIENFKRBPPIVYLIIFFWGLANGLSI 60
QY 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNWIIFGDLACRIMSISLYV 120
DB 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNWIIFGDLACRIMSISLYV 120
QY 121 NMTSSIFLTVLSVVRFLAMVHPFRLIHTSIRSAMIICGIIWILIMASSIMLLDSGSEQ 180
DB 121 NMTSSIFLTVLSVVRFLAMVHPFRLIHTSIRSAMIICGIIWILIMASSIMLLDSGSEQ 180
QY 181 NSGVTSCLELNLKIKAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NSGVTSCLELNLKIKAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHLITWVKVGCCKDRLHKALVITLALAAANCF 300
DB 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHLITWVKVGCCKDRLHKALVITLALAAANCF 300
QY 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346
DB 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346

```

RESULT 2

AAE07538 standard; protein; 346 AA.

AAE07538;

06-NOV-2001 (first entry)

Human G-protein coupled receptor 1a (GPCR1a) variant.

Human; G-protein coupled receptor; GPCR1; GPCR1a; cardiomyopathy;
atherosclerosis; hypertension; congenital heart defect; anorexia;
atrial septal defect; ventricular septal defect; valve disease;
scleroderma; obesity; transplantation; adrenoleucodystrophy; AIDS;
congenital adrenal hyperplasia; prostate cancer; lymphoma; cancer;
haemophilia; idiopathic thrombocytopenic purpura; dyslipidaemia;
acquired immune deficiency syndrome; diabetes; infectious disease;
metabolic syndrome X; Albright Hereditary Osteodystrophy; ASD; VSD;
neurodegenerative disorder; Alzheimer's disease; immune disorder;
fertility; Parkinson's disorder; haematopoietic disorder.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..59 /label= Signal_peptide

Protein 60..346 /label= Mature_human_GPCR1a_protein_variant

MO200159113-A2.

16-AUG-2001.

08-FEB-2001; 2001WO-US004404.

08-FEB-2000; 2000US-0180929P.

09-FEB-2000; 2000US-0181045P.

09-FEB-2000; 2000US-0181339P.

09-FEB-2000; 2000US-0181344P.

17-FEB-2000; 2000US-0183392P.

20-JUL-2000; 2000US-0219585P.

20-JUL-2000; 2000US-0219758P.

26-JUL-2000; 2000US-0221341P.

XX (CURA-) CURAGEN CORP.

XX Taupier RJ, Burgess CE, Padigaru M, Tchernev VT, Mishra VS;

PI Casmen S, Ballinger R, Vernet CAM, Li L, Spytek KA, Andrew DP;

PI Mezes PS;

DR MPI; 2001-497077/54.

DR N-PSDB; AAD13709.

PT Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful for

PT treating or preventing, e.g., cardiomyopathy, atherosclerosis,

PT hypertension, acquired immune deficiency syndrome, bronchial asthma,

PT Crohn's disease, and multiple sclerosis.

XX Claim 1, Page 6, 135pp; English.

XX The invention relates to human G-protein coupled receptor proteins 1-7

CC (GPCR1-7 or GPCRX) and nucleic acid molecules encoding such proteins.

CC GPCR sequences are used to treat or prevent a human suffering from GPCR

CC -associated disorders, e.g. cardiomyopathy, atherosclerosis,

CC hypertension, congenital heart defects, aortic stenosis, atrial septal

CC defect (ASD), atriocentricular (A-V) canal defect, ductus arteriosus,

CC pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD),

CC valve diseases, tuberculous sclerosis, scleroderma, obesity,

CC transplantation, adrenoleucodystrophy, congenital adrenal hyperplasia,

CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer,

CC fertility, haemophilia, hypercoagulability, idiopathic thrombocytopenic

CC purpura, graft versus host disease, acquired immune deficiency syndrome

CC (AIDS), bronchial asthma, Crohn's disease, multiple sclerosis, and

CC treatment of Albinism Hereditary Osteodystrophy. GPCR antibodies are

CC used to treat a pathological state and treat or prevent disorders such as

CC diabetes, metabolic disturbances associated with obesity, metabolic

CC syndrome X, anorexia, wasting disorders associated with chronic diseases,

CC infectious disease, cancer-associated cachexia, cancer, neurodegenerative

CC disorders, Alzheimer's disease, Parkinson's disorder, immune disorders,

CC haematopoietic disorders and various dyslipidaemias. GPCR DNA is also

CC useful in gene therapy. The present sequence is human GPCR1a protein

CC variant

XX Sequence 346 AA;

XX Query Match 100.0%; Score 1788; DB 4; Length 346;

Best Local Similarity 100.0%; Pred. No. 2.7e-180;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MERKMSLOPSISVSEMEBNGTFSNNRNCTIENFKRBPPIVYLIIFFWGLANGLSI 60
DB 1 MERKMSLOPSISVSEMEBNGTFSNNRNCTIENFKRBPPIVYLIIFFWGLANGLSI 60
QY 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNWIIFGDLACRIMSISLYV 120
DB 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNWIIFGDLACRIMSISLYV 120
QY 121 NMTSSIFLTVLSVVRFLAMVHPFRLIHTSIRSAMIICGIIWILIMASSIMLLDSGSEQ 180
DB 121 NMTSSIFLTVLSVVRFLAMVHPFRLIHTSIRSAMIICGIIWILIMASSIMLLDSGSEQ 180
QY 181 NSGVTSCLELNLKIKAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NSGVTSCLELNLKIKAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHLITWVKVGCCKDRLHKALVITLALAAANCF 300
DB 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHLITWVKVGCCKDRLHKALVITLALAAANCF 300
QY 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346
DB 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346

```

ID AAU07294 standard; protein; 346 AA.
 XX
 AC AAU07294;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Cysteineyl leukotriene receptor HIPHM0000007.
 XX
 KM Cysteineyl leukotriene receptor; HIPHM0000007; antiaesthetic; antihiv;
 KM antiallergic; antiinflammatory; antiarteriosclerotic; antiarrhythmic;
 KM vasotrophic; cytosolic; neuroprotective; antineurotic; antiaesthetic;
 KM immunosuppressive; antipsoriatic; dermatological; antibacterial;
 KM cerebroprotective; antihypertensive; asthma; allergic rhinitis; AIDS;
 KM cardiac arrhythmia; myocardial ischemia; atherosclerosis; heart failure;
 KM rheumatoid arthritis; immune disorder; dermatitis; septic shock; stroke.
 XX
 OS Homo sapiens.
 XX
 PN WO200159105-A1.
 XX
 PD 16-AUG-2001.
 XX
 PF 12-FEB-2001; 2001WO-GB000560.
 XX
 PR 10-FEB-2000; 2000GB-00003079.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Couvrens DJ, Volpe F, Ignar DM;
 XX
 DR WPI; 2001-514666/56.
 XX
 DR N-PSDB; AAS10778.
 XX
 PT Novel cysteineyl leukotriene receptor polypeptide, termed as HIPHM0000007
 PT polypeptide, useful for treating cardiovascular diseases, lung diseases,
 PT allergic rhinitis, immune deficiency and disorder.
 XX
 PS Claim 1; Page 47-48; 52pp; English.
 XX
 CC The sequence represents the amino acid sequence of cysteineyl leukotriene
 CC receptor polypeptide, termed as HIPHM0000007. The nucleic acid is useful
 CC for identifying a substance that modulates cysteineyl leukotriene receptor
 CC activity. This substance is useful for treating a subject having a
 CC disorder which is responsive to cysteineyl leukotriene receptor
 CC modulation, such as asthma, chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, cardiac arrhythmia, myocardial ischemia,
 CC atherosclerosis and heart failure. It is also useful in the therapeutic
 CC treatment and/or prophylaxis of disorders such as acquired immune
 CC deficiency syndrome (AIDS), rheumatoid arthritis, multiple sclerosis,
 CC leukemia, myasthenia gravis, Grave's disease, systemic lupus
 CC erythematosus, inflammatory bowel disease, encephalomyelitis, psoriasis,
 CC atopic dermatitis, septic shock, stroke and ischemia reperfusion injury.
 CC The antibody to cysteineyl leukotriene receptor is useful for
 CC immunoprecipitation techniques, as tools to further elucidate the
 CC function of HIPHM0000007 or its variant, and as therapeutic agent. The
 CC nucleic acid is useful for identifying mutations in HIPHM0000007 gene
 CC implicated in human disorders, which is in turn useful for diagnosing the
 CC disorder or susceptibility to the disorder and in assessing the
 CC physiology of the disorders. It is also useful in hybridisation studies
 CC to monitor up- or down-regulation of HIPHM0000007 expression
 XX
 SQ Sequence 346 AA;
 XX
 Query Match 100.0%; Score 1788; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-180;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MERKFMALOPSISISEMERNPTSPNNNSRNTIENFKRGEPPPIYLLIFWGVLTGSLT 60
 QY 61 YVFLQPKKSTSVNVFMNLALISDLLFISTLPPRADYYLRGSMWIFGDLACRIMSSTLYV 120
 DB 61 YVFLQPKKSTSVNVFMNLALISDLLFISTLPPRADYYLRGSMWIFGDLACRIMSSTLYV 120

DB 61 YVFLQPKKSTSVNVFMNLALISDLLFISTLPPRADYYLRGSMWIFGDLACRIMSSTLYV 120
 QY 121 NMTSSIFELTVLSVRFPLAMVHPFLLHTSIRSANILGIIWILMASSIMLLDSGSEQ 180
 DB 121 NMTSSIFELTVLSVRFPLAMVHPFLLHTSIRSANILGIIWILMASSIMLLDSGSEQ 180
 QY 181 NGSVTSCLEINLYKIKLQTMNYIALVGCILPPEFTLSICVLLIIVLKVPEPGLRV 240
 DB 181 NGSVTSCLEINLYKIKLQTMNYIALVGCILPPEFTLSICVLLIIVLKVPEPGLRV 240
 QY 241 SHRKALTTITITLIFELCPYHTLRTVHLATWKGCLCKDRHLKALVITLALANACP 300
 DB 241 SHRKALTTITITLIFELCPYHTLRTVHLATWKGCLCKDRHLKALVITLALANACP 300
 QY 301 NPLLYFAGENFKDLKSAIRKQHPQAKTKCVFVSVWLKRETRV 346
 DB 301 NPLLYFAGENFKDLKSAIRKQHPQAKTKCVFVSVWLKRETRV 346
 RESULT 4
 AAB82852
 ID AAB82852 standard; protein; 346 AA.
 XX
 AC AAB82852;
 XX
 DT 12-NOV-2001 (first entry)
 XX
 DE Human P2Y-1like GPCR protein.
 XX
 KM P2Y-1like; G-protein coupled receptor; GPCR; human;
 KM cysteineyl leukotriene receptor; cyclin LTD4; bactericide; fungicide;
 KM protozoacide; virucide; analgesic; cytosolic; anabolic; antiaesthetic;
 KM antiparkinsonian; cardiac; hypertensive; hypotensive; osteopathic;
 KM antilicer; immunosuppressive; antiallergic; antisclerotic;
 KM neuroprotective; antipsychotic; therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Location/Qualifiers
 FT 41..63
 FT /label= TM1
 FT /note= "transmembrane domain 1"
 FT 77..96
 FT /label= TM2
 FT /note= "transmembrane domain 2"
 FT 114..137
 FT /label= TM3
 FT /note= "transmembrane domain 3"
 FT 156..173
 FT /label= TM4
 FT /note= "transmembrane domain 4"
 FT 202..223
 FT /label= TM5
 FT /note= "transmembrane domain 5"
 FT 249..266
 FT /label= TM6
 FT /note= "transmembrane domain 6"
 FT 296..313
 FT /label= TM7
 FT /note= "transmembrane domain 7"
 FT
 PN WO200168842-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-EP002785.
 XX
 PR 14-MAR-2000; 2000US-0189045P.
 XX
 PA (PARB) BAYER AG.
 XX
 PI Xiao Y;
 XX

Db 181 NGSVTSCLSLNLYKIALQTMNYIALVVGCLPFTLSICYLIIIRVLKVEVPSGLRV 240
QY 241 SHRKALTTIIITIIIFLFCPLPYHTLTHTLTKVGLCKDRILKALVITLALAAANACF 300
Db 241 SHRKALTTIIITIIIFLFCPLPYHTLTHTLTKVGLCKDRILKALVITLALAAANACF 300
QY 301 NPLLYYFAGENFDRILKSLARKGHPQAKTKCVFVSWMLRKETRV 346
Db 301 NPLLYYFAGENFDRILKSLARKGHPQAKTKCVFVSWMLRKETRV 346
RESULT 6
AAE12022
ID AAE12022 standard; protein; 346 AA.
AC AAE12022;
XX
XX 18-DEC-2001 (first entry)
DE Human G-protein coupled receptor; GCRC-1.
XX
XX Human G-protein coupled receptor; GCRC; gene therapy;
KM proteosome analysis; cell proliferative disorder; arteriosclerosis;
KM cancer; neurological disorder; Huntington's disease; Parkinson's disease;
KM cardiovascular disorder; atherosclerosis; congestive heart failure;
KM gastrointestinal disorder; gastritis; nausea; autoimmune; anaemia;
KM inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
KM metabolic disorder; diabetes; obesity; viral infection; drug screening;
KM chromosomal mapping; cytostatic; immunomodulatory; anti-inflammatory;
viralicide.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..55
FT /label= signal_peptide
FT Domain 38..61
FT /label= Transmembrane_domain
FT Protein 56..346
FT /note= "Mature human GCRC-1 protein"
FT Domain 198..221
FT /label= Transmembrane_domain
XX
XX MO200172836-A2.
XX
XX 04-OCT-2001.
PD
XX 29-MAR-2001; 2001WC-US010436.
PF
XX 29-MAR-2000; 2000US-0193051P.
PR 06-APR-2000; 2000US-0195155P.
PR 20-APR-2000; 2000US-0199084P.
PR 28-APR-2000; 2000US-0200551P.
PR 05-MAY-2000; 2000US-0202278P.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Policky JL, Tribouley CM, Tang YT, Baughn MR, Graul R, Khan FA,
PI Nguyen DB, Patterson C, Lal P, Au-Young J, Yang J, Hatalla A;
PI Wella NK, Das D;
XX
XX WPI, 2001-616472/71.
DR N-PSDB; AAD19577.
XX
XX New human G-protein coupled receptors, useful for treatment and diagnosis
PT of e.g. cell proliferation, also screening for specific modulators, and
XX related nucleic acid.
XX
XX Claim 1, Page 101-102, 11pp; English.
XX
XX The present sequence is a human G-protein coupled receptor, GCRC-1
CC protein. The GCRCs are used for treating or preventing disorders
CC associated with decreased expression of functional GCRC, and for

CC identifying specific agonists and antagonists, also binding agents and
CC modulators. They can also be used for generating specific antibodies and
CC for proteosome analysis. Disorders that can be treated include cell
CC proliferative disorders, e.g., arteriosclerosis and cancer, neurological
CC disorders, e.g., Huntington's disease and Parkinson's disease,
CC cardiovascular disorders, e.g., atherosclerosis and congestive heart
CC failure, gastrointestinal disorders, e.g., gastritis and nausea,
CC autoimmune/inflammatory disorders, e.g., acquired immunodeficiency
CC syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and
CC obesity and viral infections. Nucleic acids that encode GCRC are used
CC for identifying agents that alter its expression, for assessing toxicity
CC of test compounds and as sources of primers and probes for diagnostic
CC detection of GCRC DNA and of therapeutic antisense and ribozyme
CC sequences. They can also be used in gene therapy, for chromosomal
CC mapping, and for recombinant production of GCRC. The antibodies are
CC useful for diagnosis and monitoring of diseases associated with GCRC
CC expression, for detecting and purifying GCRC, and as therapeutic agents
CC and for drug screening
XX
XX Sequence 346 AA;
SQ
Query Match 100.0%; Score 1788; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 2,7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNTIENKREFFPIVYLIIFPMGVLAGNLSI 60
Db 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNTIENKREFFPIVYLIIFPMGVLAGNLSI 60
QY 61 YVFLQPKYSTSVNVMNLAIISDLFIETLPRADYVLRGSWITGDLACRIMSYSLVY 120
Db 61 YVFLQPKYSTSVNVMNLAIISDLFIETLPRADYVLRGSWITGDLACRIMSYSLVY 120
QY 121 NMTSIVFLTVLSVVFLLAVHVFRLHVTISIRSAMILGIIWILMASSIMLDSGSEQ 180
Db 121 NMTSIVFLTVLSVVFLLAVHVFRLHVTISIRSAMILGIIWILMASSIMLDSGSEQ 180
QY 181 NGSVTSCLSLNLYKIALQTMNYIALVVGCLPFTLSICYLIIIRVLKVEVPSGLRV 240
Db 181 NGSVTSCLSLNLYKIALQTMNYIALVVGCLPFTLSICYLIIIRVLKVEVPSGLRV 240
QY 241 SHRKALTTIIITIIIFLFCPLPYHTLTHTLTKVGLCKDRILKALVITLALAAANACF 300
Db 241 SHRKALTTIIITIIIFLFCPLPYHTLTHTLTKVGLCKDRILKALVITLALAAANACF 300
QY 301 NPLLYYFAGENFDRILKSLARKGHPQAKTKCVFVSWMLRKETRV 346
Db 301 NPLLYYFAGENFDRILKSLARKGHPQAKTKCVFVSWMLRKETRV 346
RESULT 7
AAE17231
ID AAE17231 standard; protein; 346 AA.
XX
XX AAE17231;
AC
XX 07-MAY-2002 (first entry)
DT
XX Human CybL72 GPCR (G-protein coupled receptor).
DE
XX
XX Human CybL72 GPCR (G-protein coupled receptor).
DE
XX
XX Human, CybL72 GPCR, G-protein coupled receptor; oedema; asthma;
KM immunological disorder; vascular disorder; reproductive disease;
KM cellular metabolism; growth; development; blood; bone homeostasis;
KM inflammation; allergy; angiogenesis; respiratory distress syndrome;
KM Crohn's disease; blood pressure; protein therapy; anti-inflammatory;
KM inflammatory disorder.
XX
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 1..41
FT /label= Extracellular_domain
FT Modified-site 20..22

Query Match	100.0%	Score 1788	DB 5	Length 346
Best Local Similarity	100.0%	Pred. No. 2.7e-180		
Matches 346	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Sequence 346 AA				
Query Match				
Best Local Similarity	100.0%	Pred. No. 2.7e-180		
Matches 346	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Sequence 346 AA				

Db	241	SHRKALTTTITITLITLIFPCLCPYHTLRTVHLITWVGVGCKQRLKHALVITLTLAANAACP	300
Qy	301	NPRLYYFAGENFKDRLKSLARKGHPQAKTKCVFVSVLWLRKERTV	346
Db	301	NPRLYYFAGENFKDRLKSLARKGHPQAKTKCVFVSVLWLRKERTV	346
RESULT 8			
AAAG77965			
XX	ID	AAAG77965 standard; protein; 346 Aa.	
XX	AC	AAAG77965;	
XX	DT	25-FEB-2002 (first entry)	
XX	DE	Human G-protein coupled receptor PFI-017*.	
KW	XX	Human; G-protein coupled receptor; GPCR; PFI-017*; cytostatic;	
KW	KW	antiallergic; osteopathic; cardiovascular; immunosuppressive; neoplastic;	
KW	KW	gene therapy; heart disease; gastrointestinal disease; sleep disorder;	
KW	KW	immunological disorder; pulmonary disorder; infectious disease;	
KW	KW	myeloproliferative disease; allergic rhinitis; asthma; COPD; obesity;	
KW	KW	chronic obstructive pulmonary disease; inflammatory bowel disease;	
KW	KW	diabetes; metabolic disease; neurological disease; urogenital disease;	
KW	KW	inflammation; cancer; osteoporosis; cardiovascular disease; infection;	
KW	KW	allergy; respiratory disease; sensory organ disorder; hair loss;	
KW	KW	immunological disorder; pulmonary disease; neoplastic disease;	
KW	KW	vasculitic granulomatous disease; dermatology; psychotherapeutic.	
XX	OS	Homo sapiens.	
XX	PN	US2001039037-A1.	
XX	PD	08-NOV-2001.	
XX	XX	05-APR-2001; 2001US-00826791.	
XX	XX	05-APR-2000; 2000GB-00008504.	
XX	XX	19-APR-2000; 2000US-0198367P.	
XX	XX	(HARL.) HARLAND L.	
XX	PI	Harland L;	
XX	DR	WPI: 2002-040722/05.	
XX	DR	N-PSDB; AAH77279.	
XX	XX	New PFI-017 protein and polynucleotide encoding the protein, useful for	
XX	XX	diagnosing or treating metabolic diseases, urogenital disease,	
XX	XX	immunological disorders, infectious diseases, , neoplastic or	
XX	XX	myeloproliferative diseases.	
XX	XX	Claim 7, Fig 7B; 39pp; English.	
CC	CC	The sequence represents a novel G-protein coupled receptor (GPCR), PFI-	
CC	CC	017* of the invention. The PFI-017 has cytostatic, antiallergic,	
CC	CC	osteopathic, cardiovascular, and immunosuppressive activity. The	
CC	CC	polynucleotides may have a use in gene therapy. The polynucleotide is	
CC	CC	useful for treating allergic disorders, an inflammatory disorder, an	
CC	CC	immunological disorder, a pulmonary disorder, an infectious disease, a	
CC	CC	neoplastic or myeloproliferative disease, or a heart disease. The	
CC	CC	allergic disorder is an allergic rhinitis or asthma, the pulmonary	
CC	CC	disease is COPD, and the inflammatory disorder is inflammatory bowel	
CC	CC	disease. PFI-017 polynucleotide sequences may be used for the diagnosis	
CC	CC	of diseases resulting from expression of PFI-017, and to detect and	
CC	CC	quantify gene expression in conditions, disorders or diseases in which	
CC	CC	PFI-017 activity may be implicated. The polypeptides are used to produce	
CC	CC	anti-PFI-017 antibodies to be used diagnostically to detect and quantify	
CC	CC	PFI-017 levels in disease states. The antibodies, compounds and	
CC	CC	compositions which can modulate the peptide can be used in treating	
CC	CC	obesity, diabetes and metabolic disease, neurological disease, urogenital	
CC	CC	disease, inflammation, cancer, osteoporosis, cardiovascular disease,	

CC gastrointestineal disease, infections, allergy and respiratory disease,
CC sensory organ disorders, sleep disorders, hair loss, immunological
disorders, pulmonary diseases, infectious diseases, neoplastic and
CC myeloproliferative diseases, vasculitic granulomatous diseases, and heart
CC diseases. These may also be used in dermatology, and psychotherapeutics
XX
XX Sequence 346 Aa,
Aa

SQ Sequence 346 AA;

```

Query Match      .      100.0%      Score 1788:  DB 5      Length 346;
Best Local Similarity 100.0%      Pred. Nc. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels _ 0; Gaps 0;

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QY 1 MERKMSLQGISVSSEMEPNGTFSNNNSRNTIENFKREFFPIVLLIFPWGLGNGLSI 60
    |||||
Db 1 MERKMSLQGISVSSEMEPNGTFSNNNSRNTIENFKREFFPIVLLIFPWGLGNGLSI 60

```

Qy 61 YVFLQPKKSTSVNFMNLAIISDLLFISTLPFRADYYLRGSNWI FGLACRIMSYSLV 120
 |||||
Db 61 YVFLQPKKSTSVNFMNLAIISDLLFISTLPFRADYYLRGSNWI FGLACRIMSYSLV 120

Db 121 NMYSITFLIVLSVVRFLAMVHPRLIHVTSIRSAWILCGITWILIMASSIMLDSGSEQ 180C

181 NGSVTSCLBNLYKIAKQTNNYIALVGCILPFTLSICYLLIRVLKVEVPESGRV 240
 182 |||||
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241 SHRKALTTITLLIFFLCPHYHTRTVHLTWKVGCKDKRLKALVITLMAAANCF 3000

Oy	301 NPLLYFAGENFKDRLKSALEKGHPQAKTKCVPEVSVMLRKETRV	3466
Db	301 NPLLYFAGENFKDRLKSALEKGHPQAKTKCVPEVSVMLRKETRV	3466

RESULT 9
ABP95624
ID ABP95624 standard; protein; 346 AA

AC	ABP95624;
XX	
DT	06-MAR-2003 (first entry)

De XX KW	Human GPCR polypeptide SEQ ID NO 58.	Human, GPCR; G protein coupled receptor; signal transduction; olfactory

XX Homo sapiens.
OS
XX

XX 28-FEB-2002.
PD
XX
PE 30-TT-2001, 2001WO-TB001446

XX 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
PR
XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP
XX
XX
PI Haga T, Takeda S, Mitaku S;
XX

DR	N-PSDB; ABZ42898.
XX	
PT	Database global search

Claim 10; SEQ ID NO 58; 97pp + Sequence Listing; Japanese.

XX The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (AB242870-AB24216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 346 AA;

SQ Sequence 346 AA;

Query Match	100.0%	SCORE 1788; DB 5;	Length 346;
Best Local Similarity	100.0%	Pred. No. 2.7e-180;	
Matches 346; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0

Db
OY
1 MERKMSLOPSISVSEMEPNNGTFSNNNSRNTIENFKRBEPIVLLIFPMGVLGSLI 60
1 MERKMSLOPSISVSEMEPNNGTFSNNNSRNTIENFKRBEPIVLLIFPMGVLGSLI 60

61 YVFLQPIKKSISVANVELMLAISLLFLISLPEFADYLRNGSNMFLPGDLACRIMSSLSLV 120

QY 121 NMYSIYFLTVLSYRFLAMVHPRLLHTYSIRSAWILCGIWIWIMASSIMLDGSGEQ 180

QY 181 NGASTSCLELNLYKIAKOTMNYIALVVGCLPFFTLSCYLLIRVLKKEVPESGLRV 240

Db 181 NGASTSCLELNLYKIAKOTMNYIALVVGCLPFFTLSCYLLIRVLKKEVPESGLRV 240

Db

241 SHRAATLTIIITLIFELCFPHYTLVHLLTWKVGCLCKDRMLHQLVITLALANNAFC 300

Db 301 NPLLYFAGENFKDRLSALRKGPQKAKTKCVFVSVMLRKETRV 346

RESULT 10
ABG66684
ID ABG66684 standard; protein; 346 AA

AC	ABG66684;
XX	
DT	30-AUG-2002 (first entry)
DT	

DE	Human novel polypeptide #19
XX	
KW	Human; inflammatory condition
KW	Human; inflammatory condition

KW	peripheral n
KW	myeloid cell
KW	cartilage; 1
KW	bone degener

KW	lung fibrosis;
KW	allergic condit
KW	fungal infectio
XX	

OS HOMO BAPTENS
XX
PN WO200244340-
XX

XX	30-NOV-2001; 2001WO-US047004
XX	
XX	

PR 30-NOV-2000; 2000US-00728952.
XX (HYSE-) HYSEQ INC.
PA Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D,
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX MPI; 2002-508509/54.
DR N-PSDB; ABK94908.
XX
PT Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT disorders, cancer and promoting wound healing.
XX
XX Claim 10; Page 582-583; 672pp; English.
XX
XX The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic
CC and coagulation disorders. Sequences ABG6666-ABG66758 represent human
CC novel polypeptides of the invention
XX
XX Sequence 346 AA:
SO
Query Match 100.0%; Score 1788; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERKMSLOPSTISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60
DB 1 MERKMSLOPSTISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60
QY 61 YVFLQPYKSTSVNVFMNLAIISDLFIITLPPRADYLRGSNWIRGDLACRIMSGLV 120
DB 61 YVFLQPYKSTSVNVFMNLAIISDLFIITLPPRADYLRGSNWIRGDLACRIMSGLV 120
QY 121 NMYSSYFLTVLSVAFELAMVHPRLLHVTSSRSANILCGIIMILIMASSIMLDGSGSQ 180
DB 121 NMYSSYFLTVLSVAFELAMVHPRLLHVTSSRSANILCGIIMILIMASSIMLDGSGSQ 180
QY 181 NSSVSCLELNLYKIAKQTMNYIALVGCCLPFFTLSTCYLLIRVLAKVEPSGLRV 240
DB 181 NSSVSCLELNLYKIAKQTMNYIALVGCCLPFFTLSTCYLLIRVLAKVEPSGLRV 240
QY 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTVMKGLCKDRHLKALVTTLAANACF 300
DB 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTVMKGLCKDRHLKALVTTLAANACF 300
QY 301 NPLLYFAGENFKDRISALRKGHPOKATKCVFPVSWLRKRETV 346
DB 301 NPLLYFAGENFKDRISALRKGHPOKATKCVFPVSWLRKRETV 346

RESULT 11
AB05229

ID ABB05229 standard; protein; 346 AA.
XX ABB05229;
AC
XX 03-APR-2002 (first entry)
DT
XX Human LTD4-like G protein-coupled receptor protein SEQ ID NO:2.
DE
XX Human, LTD4-like G protein-coupled receptor; LTD4-like GPCR; antifungal;
KW antibacterial; antiviral; protozoacide; analgesic; cytosolic; cardiant;
KW hypotensive; hypertensive; antiangiinal; anorectic; anti-ulcer; nootropic;
KW antiallergic; antiallergic; antileptine; antileptic; anticonvulsant;
KW immunostimulant; neuroprotective; neuroleptic; osteopathic; anti-HIV;
KW gene therapy; vaccine; infection; pain; cancer; diabetes; obesity;
KW anorexia; acute heart failure; hypotension; hypertension; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy;
KW benign prostatic hypertrophy; migraine; vomiting; dementia; dyskinesia;
KW severe mental retardation; Huntington's disease; immunological response;
KW Gilles de la Tourette's syndrome.
XX
OS Homo sapiens.
XX
XX WO200194580-A1.
PN
XX 13-DEC-2001.
PD
XX 02-JUN-2001; 2001WO-BP006313.
PF
XX 06-JUN-2000; 2000EP-00112147.
PR
XX (MERS) MERCK PATENT GMBH.
XX
PA Kluxen F, Duecker K;
PI
XX WPI; 2002-130593/17.
DR
XX N-PSDB; ABA92899.
XX
PT New LTD4 receptor like G-protein coupled receptor polypeptide and
PT polynucleotide, useful in diagnostic assays and in identifying agonists
PT or antagonists for treating infections, pain, cancer, hypertension,
PT stroke, ulcers or asthma.
XX
PS Claim 1; Page 40; 43pp; English.
XX
XX The present sequence represents the human LTD4-like G protein-coupled
CC receptor (GPCR) protein (I). (I) and the polynucleotide (II) encoding it
CC have antifungal, antibacterial, antiviral, protozoacide, analgesic,
CC cytosolic, cardiant, hypotensive, hypertensive, antiangiinal, anorectic,
CC anti-ulcer, antiallergic, antiallergic, antileptine, antileptic,
CC muscular, nootropic, anticonvulsant, immunostimulant, neuroprotective,
CC neuroleptic, osteopathic and anti-HIV activities, and can be used in gene
CC therapy and vaccine production. (I) and (II) can be used in diagnostic
CC assays. They can also be used in identifying compounds that may be
CC agonists or antagonists that are potentially useful in therapy, e.g. for
CC treating bacterial, fungal, protozoan or viral infections (e.g. HIV-1),
CC pain, cancer, diabetes, obesity, anorexia, acute heart failure,
CC hypotension, hypertension, osteoporosis, angina pectoris, myocardial
CC infarction, stroke, ulcer, asthma, allergies, benign prostatic
CC hypertrophy, migraine, vomiting, dementia, or severe mental retardation
CC or dyskinesias (e.g. Huntington's disease or Gilles de la Tourette's
CC syndrome). (I) and (II) can also be used in vaccines for inducing an
CC immunological response in a mammal
XX
XX Sequence 346 AA;
SO
Query Match 100.0%; Score 1788; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERKMSLOPSTISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60
DB 1 MERKMSLOPSTISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60

Oy		61	VVFLOPYPKKSTSVNPMNLIALSDLLFIETLPPRAADYYIARGSWITGDLACRIMSYSLYV	120
Db		61	VVFLOPYPKKSTSVNFMNLIALSIDLLFIETLPPRAADYYIARGSWITGDLACRIMSYSLYV	120
Oy		121	NMYSIIYFLTVASVVRFLAMWHPFRLLAHTSIRSANILGGIIVILLMASSIMLDGSEQ	180
Db		121	NMYSIIFLTUVASVRFLLAMWHPFRLLAHTSIRSANILCGIIVILLMASSIMLDGSEQ	180
Oy		181	NGSVTSCELANLYKIAKLOTMYALAVGCGLPEFTLSICYLHIIHVLLKEVEPEGSLRV	240
Db		181	NGSVTSCEELNLYKIAKLOTMYALAVGCGLPEFTLSICYLHIIHVLLKEVEPEGSLRV	240
Oy		241	SHRKALLTIIITLIIFLCFPLPHYTRRTYHLTWKVGCLKDRHKALVTTLAAANACP	300
Db		241	SHRKALLTIIITLIIFLCFPLPHYTRRTYHLTWKVGCLKDRHKALVTTLAAANACP	300
Oy		301	NPLYVPAGENFKDRLKSALRGKHPOKATKCVPSPVSWLRKETRV	346
Db		301	NPLYVPAGENFKDRLKSALRGKHPOKATKCVFPSPVSWLRKETRV	346
RESULT 12				
ID	AAU10004		standard; protein; 346 AA.	
XX	AAU10004;			
XX				
DT	18-JUN-2002	(first entry)		
XX				
DE		Human CysLT2-like G-protein coupled receptor protein.		
XX				
KW	CysLT2; G-protein coupled receptor; GPCR; cysteinyl leukotriene2;			
KW	antibacterial; fungicide; virucide; cytostatic; anti-HIV; antitubungal;			
KW	hypertensive; hypertensive; osteopathic; tranquiliser; nootropic;			
KW	anti-inflammatory; neuroprotective; antiparkinsonian; analgesic;			
KW	cardiac; cerebroprotective; antilactamic; antiallergic; antiarthritis;			
KW	antifluor; antibody; immunogen; bacterial infection; fungal infection;			
KW	viral infection; human immunodeficiency virus; HIV; cancer; anorexia;			
KW	bulimia; cardiovascular disease; acute heart failure; angina;			
KW	myocardial infarction; ulcer; osteoporosis; asthma; allergy; neurogenic;			
KW	myopathic; neurodegenerative; Alzheimer's disease; Parkinson's disease;			
KW	motor neuron disease; dementia; inflammatory disease; arthritis;			
KW	multiple sclerosis; human.			
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	Domain	41..63	/note= "Transmembrane helix"	
FT	Domain	77..96	/note= "Transmembrane helix"	
FT	Domain	93..110	/note= "Transmembrane helix"	
FT	Region	104..143	/note= "Transmembrane helix"	
FT	Region	113..137	/note= "GPCR region"	
FT	Domain	115..139	/note= "Transmembrane helix"	
FT	Domain	156..173	/note= "Transmembrane helix"	
FT	Domain	202..223	/note= "Transmembrane helix"	
FT	Region	210..221	/note= "Transmembrane helix"	
FT	Region	241..268	/note= "GPCR region"	
FT	Region	250..266	/note= "GPCR region"	
FT	Domain	291..313	/note= "Transmembrane helix"	
FT	Domain	297..308	/note= "Transmembrane helix"	
FT	Region		/note= "GPCR region"	

XX	FN	WO200177149-A2.
XX	PD	18-OCT-2001.
XX	PF	06-APR-2001; 2001WO-EP003981.
XX	PR	07-APR-2000; 2000US-0195196P.
XX	PT	13-DEC-2000; 2000US-0254876P.
XX	PS	(FARB) BAYER AG.
XX	PI	Xiao Y;
XX	DR	WPI; 2002-049130/06.
XX	DR	N-PsDB; AAS16243.
XX	PT	New polypeptide, useful for treating peripheral or central nervous
XX	PT	system, cardiovascular diseases and asthma, comprises the human
XX	PT	cysteinyllenkotrien2-1ike G protein-coupled receptor polypeptide.
XX	PS	Claim 25; Fig 9; 136pp; English.
XX	PS	This sequence represents a human CysLT2-like G-protein coupled receptor
XX	CC	(GPCR) protein of the invention. The invention comprises the DNA and
XX	CC	protein sequences of an isolated human CysLT2 (cysteinyllenkotrien2)-
XX	CC	like G protein-coupled receptor (GPCR) protein. This protein may have
XX	CC	antibacterial, fungicide, virucide, cytostatic, anti-HIV, antiangiinal,
XX	CC	hypotensive, hypertensive, osteopathic, tranquiliser, nootropic, anti-
XX	CC	inflammatory, neuroprotective, antiparkinsonian, analgesic, cardiant,
XX	CC	cerebroprotective, antialstematic, antiallergic, antiarthritic and
XX	CC	anticancer activities. The invention also comprises an agent which
XX	CC	inhibits the function of the CysLT2-like protein and is useful for
XX	CC	treating CysLT2-like GPCR disorders. The protein or its fragment are
XX	CC	useful in raising specific antibodies which can block ligand binding, and
XX	CC	are useful for treating disorders such as bacterial, fungal and viral
XX	CC	infections and particularly those caused by human immunodeficiency (HIV)
XX	CC	virius, cancers, anorexia, bulimia, cardiovascular diseases (e.g. acute
XX	CC	heart failure, angina, myocardial infarction), ulcers, osteoporosis,
XX	CC	asthma, allergies, central and peripheral nervous system disease, a
XX	CC	disease of the motor unit like neurogenic and myopathic disorders,
XX	CC	neurodegenerative disorders (e.g. Alzheimer's and Parkinson's disease,
XX	CC	motor neuron disease, dementia) also inflammatory diseases of the nervous
XX	CC	system (e.g. arthritis and multiple sclerosis). The coding sequence of
XX	CC	CysLT2-like GPCR polynucleotide is useful for generating antisense
XX	CC	oligonucleotides or ribozymes which specifically bind to mRNA transcribed
XX	CC	from the cysLT2 gene and are useful for modulating CysLT2-like GPCR gene
XX	CC	expression
XX	CC	Sequence 346 AA;
XX	CC	Query Match 100.0%; Score 1788; DB 5; Length 346;
XX	CC	Best Local Similarity 100.0%; Prid. No. 2.7e-180;
XX	CC	Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	CC	1 MERKFMISLOPSISVSEMEPNGTFSNNNSRNTTIEFKREPPPIYYLLIFPMGVLGNGLSI 60
XX	CC	1 MERKFMISLOPSISVSEMEPNGTFSNNNSRNTTIEFKREPPPIYYLLIFPMGVLGNGLSI 60
XX	CC	61 YVFLQPKYKSTSVNVFPMNLALISDLFISTLPFRADYYLKGSMNIFGDLACRIMSYSLLY 120
XX	CC	61 YVFLQPKYKSTSVNVFPMNLALISDLFISTLPFRADYYLKGSMNIFGDLACRIMSYSLLY 120
XX	CC	121 NMGSIIYFLTYLTVSVRFPLAMVHPRLAHVTSIRSAWILCGIITWLLMASSIMLDSGSEQ 180
XX	CC	121 NMGSIIYFLTYLTVSVRFPLAMVHPRLAHVTSIRSAWILCGIITWLLMASSIMLDSGSEQ 180
XX	CC	181 NGSYTSCIEENLKYXIALQTMNNTYALVVGCLLPFTSICYLITIRYLAKVEVSGLRV 240
XX	CC	181 NGSYTSCIEENLKYXIALQTMNNTYALVVGCLLPFTSICYLITIRYLAKVEVSGLRV 240
XX	CC	241 SHRAKLTITITITLIIFFLCPLPYHTLTFTVHLTVMKVGLCRDRLHKALVITLALAAANACF 300

Db 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKLAVITLALAAANCF 300
 QY 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346
 Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 13
 ABU11923
 ID ABU11923 standard; protein; 346 AA.
 AC ABU11923;
 XX
 DT 13-FEB-2003 (first entry)
 XX
 DE Human G-protein coupled receptor HGRPRMY11.
 XX
 KW Human; receptor; HGRPRMY11; HGRPRMY11v1; HGRPRMY11v2; GPCR74; GPCR81;
 KW G-protein coupled receptor; cardiovascular disease; arrhythmia;
 KW myocardial infarction; congestive heart failure; cardiomyopathy;
 KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;
 KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;
 KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;
 KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukemia;
 KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200286123-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 16-NOV-2001; 2001WO-US044019.
 XX
 PR 17-NOV-2000; 2000US-0249613P.
 PR 21-DEC-2000; 2000US-0257611P.
 PR 16-JUL-2001; 2001US-0305818P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LB;
 XX
 DR MPI; 2003-093137/08.
 DR N-PSDB; ABX56012.
 XX
 PT New human G-protein coupled receptor HGRPRMY11 polypeptide or
 PT polynucleotide, useful for preventing, treating or ameliorating e.g.
 PT myocardial infarction, angina, thrombosis, Alzheimer's disease,
 PT schizophrenia, AIDS, leukemia.
 XX
 PS Claim 33; Fig 6; 444p; English.
 XX
 CC The invention relates to an isolated polypeptide (designated HGRPRMY11),
 CC which has a G-protein coupled receptor (GPCR) activity (also known as
 CC GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit
 CC Number PTA-2766, its variants (HGRPRMY11v1 and HGRPRMY11v2), fragments,
 CC domains, species homologues and proteins 95% similar to it. Also included
 CC are: (1) the nucleic acids encoding the HGRPRMY11 proteins (including
 CC variants, fragments, complements and sequences 95% similar to the
 CC HGRPRMY11 nucleic acids); (2) recombinant vectors; (3) transformed host
 CC cells expressing HGRPRMY11; (4) an anti-HGRPRMY11 antibody; (5)
 CC diagnosing a pathological condition or a susceptibility to a pathological
 CC condition in a subject; (6) identifying a binding partner to the
 CC HGRPRMY11 polypeptide; (7) identifying an activity in a biological assay;
 CC (8) a process for making polynucleotide sequences encoding a gene product
 CC having altered GPCR activity; (9) a shuffled polynucleotide produced by
 CC the method of (8); and (10) screening for candidate compounds capable of
 CC binding to and/or modulating activity of a GPCR. The polypeptide or the
 CC polynucleotide is useful for preventing, treating or ameliorating a
 CC medical condition, particularly cardiovascular diseases or disorders,
 CC e.g. myocardial infarction, congestive heart failure, arrhythmias,
 CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
 CC thrombosis or hypertension). The HGRPRMY11 polypeptide or polynucleotide

CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's
 CC disease, Parkinson's disease, osteoporosis, obesity, human
 CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,
 CC acquired immunodeficiency syndrome (AIDS), leukemia, sepsis,
 CC inflammations, psoriasis, Gaucher's disease or ischaemia (many other
 CC diseases and disorders are listed in the specification). The present
 CC sequence represents an HGRPRMY11 protein (or variant)
 XX
 SQ Sequence 346 AA;
 Query Match 100.0%; Score 1789; DB 6; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.7e-180;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKPMSLQPSISVSEMEENGTFSSNNNSNCTIENPKRFPPIYVLIIFPMGLANGLSI 60
 Db 1 MERKPMSLQPSISVSEMEENGTFSSNNNSNCTIENPKRFPPIYVLIIFPMGLANGLSI 60
 QY 61 YFLOPKKSTSVNFMLNLAIISDLIFSTLPFRADYYLRGSNMIFGDLACRIMSISLYV 120
 Db 61 YFLOPKKSTSVNFMLNLAIISDLIFSTLPFRADYYLRGSNMIFGDLACRIMSISLYV 120
 QY 121 NMYSIYFLTVLSVVRFLAMVHPRLHVTSSIRSAWIIIGIWIIMASSIMLDSGSQ 180
 Db 121 NMYSIYFLTVLSVVRFLAMVHPRLHVTSSIRSAWIIIGIWIIMASSIMLDSGSQ 180
 QY 181 NSVTSQLEMLNYKAKIOTMYIALVVGCLLPFTLSIYLLIRVLKXVPPSSGLRV 240
 Db 181 NSVTSQLEMLNYKAKIOTMYIALVVGCLLPFTLSIYLLIRVLKXVPPSSGLRV 240
 QY 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKLAVITLALAAANCF 300
 Db 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKLAVITLALAAANCF 300

QY 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346
 Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 14
 ABP81707
 ID ABP81707 standard; protein; 346 AA.
 AC ABP81707;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human cysteinyl leukotriene CYS172 receptor protein SEQ ID NO:589.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; arteriosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX

CC in raising specific antibodies that can block the receptor and
CC effectively prevent ligand binding. The invention is useful in gene
CC therapy. The present sequence is human cysteinyl leukotriene (CysLT2)-
CC like GPCR protein.

XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1788; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 2, 7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEPNGTSSNNNSRNCTIENFRREFPIVYLIIFFWGVLGNGLSI 60
DB 1 MERKFMSLQPSISVSSEMEPNGTSSNNNSRNCTIENFRREFPIVYLIIFFWGVLGNGLSI 60
QY 61 YVFLQPYKXKSTSVNFMNLNLAISDLFI STLPRADYILRGSNMIFGDLACRIMSYSLYV 120
DB 61 YVFLQPYKXKSTSVNFMNLNLAISDLFI STLPRADYILRGSNMIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPRLHTSIRSAMILCGI IWLIMASSIMLLDSGSEQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPRLHTSIRSAMILCGI IWLIMASSIMLLDSGSEQ 180
QY 181 NGSVTSCLBLINLYKIAKLQTMNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRV 240
DB 181 NGSVTSCLBLINLYKIAKLQTMNYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRV 240
QY 241 SHRKALTTTIIITLIIFFLCFLPYHTLRTVHLTWKVGLCCKDRHKALVITLALAAANACF 300
DB 241 SHRKALTTTIIITLIIFFLCFLPYHTLRTVHLTWKVGLCCKDRHKALVITLALAAANACF 300
QY 301 NPLLYYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346
DB 301 NPLLYYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346

Search completed: December 13, 2004, 17:49:19
Job time : 157 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:35:53; Search time 189 Seconds

(without alignments)
1053.331 Million cell updates/sec

Title: US-09-980-049-1

Perfect score: 1788
Sequence: 1 MERKPMISLOPISIVSEMEPN.....KATKCVFVSWLRKTRV 346

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
(with first 1000 hits)
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_tramb1:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1788	100.0	346	1 CLT2_HUMAN	Q9N675 homo sapien
2	1788	100.0	346	2 AAH6160	AAH6160 homo sapi
3	1427.5	79.8	345	1 CLT2_PIG	Q95N03 mus scrofa
4	1204	67.3	309	2 Q8R528	Q8R528 mus musculu
5	1197	66.9	309	1 CLT2_MOUSE	Q92061 mus musculu
6	1187	66.4	309	1 CLT2_MOUSE	Q92459 ratu
7	567.5	31.7	339	1 CLT1_RAT	Q92458 ratu
8	563	31.5	340	1 CLT1_PIG	Q95N02 mus scrofa
9	560	31.3	352	1 CLT1_MOUSE	Q95N03 mus musculu
10	560	31.3	352	2 BAC28308	BAC28308 mus muscu
11	559	31.3	337	1 CLT1_HUMAN	Q9Y271 homo sapien
12	553	30.9	337	2 Q8IV19	Q8IV19 homo sapien
13	487.5	27.1	337	1 GP80_HUMAN	Q96P68 homo sapien
14	484.5	27.1	337	1 Q8N557	Q8N557 homo sapien
15	481.5	26.9	339	2 Q8N557	Q8N557 homo sapien
16	479	26.8	337	2 Q6Y1R5	Q6Y1R5 ratu
17	479	26.8	337	2 AAP32736	AAP32736 ratu
18	477	26.7	347	2 Q7Z2A4	Q7Z2A4 brachydanio
19	473.5	26.5	349	2 Q6P852	Q6P852 xenopus tro
20	473.5	26.5	349	2 AAH61378	AAH61378 xenopus t
21	473	26.5	362	1 P2YR_MEIGA	P49652 melesgri
22	470	26.3	362	1 P2YR_CHICK	P49652 gallus galli
23	468	26.2	337	2 Q6IYF8	Q6IYF8 mus musculu
24	468	26.2	337	2 AAT10591	AAT10591 mus muscu
25	463.5	25.9	361	2 Q90X57	Q90X57 xenopus lae
26	459.5	25.7	339	2 Q6N865	Q6N865 mus musculu
27	459.5	25.7	339	2 AAH70439	AAH70439 mus muscu
28	457	25.6	357	2 Q9DE05	Q9DE05 raja erinac
29	456	25.5	249	2 Q6S9C7	Q6S9C7 chinchilla
30	456	25.5	249	2 AAR26537	AAR26537 chinchilla
31	454	25.4	373	1 P2YR_CAVPO	P59902 cavia porce

ALIGNMENTS

ALIGNMENTS				
RESULT 1				
CLT2_HUMAN	STANDARD;	PRT;	346 AA.	
32	449.5	25.1	357	2 Q7TMV7
33	447.5	25.0	370	1 P2YR_HUMAN
34	447	25.0	308	1 P2YR_CHICK
35	447	25.0	373	1 P2YR_RAT
36	446	24.9	373	1 P2YR_HUMAN
37	443.5	24.8	370	2 Q6N8P5
38	443.5	24.8	370	2 AAH69996
39	442	24.7	373	1 P2YR_BOVIN
40	442	24.7	373	1 P2YR_MOUSE
41	442	24.7	373	2 BAC28413
42	442	24.7	373	2 BAC29506
43	440	24.6	361	1 EB12_HUMAN
44	439	24.6	373	2 Q8BMD5
45	437	24.4	344	1 P2YR_HUMAN

Q7TMV7 mus masculin
Q96777 mus sapien
P32250 gallus galli
P49651 rattus norv
P47900 homo sapien
Q6n8p5 homo sapien
AAh69996 homo sapi
P48042 bos tauru
P49650 mus musculu
Bac28413 mus muscu
Bac29506 mus muscu
P32249 homo sapien
Q8bmd5 mus musculu
P43657 homo sapien

CLT2_HUMAN
Q9NS75; Q9HC02;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cysteiny] leukotriene receptor 2 (CysLTR2) (P5EC0146) (HG57) (HBN321)
De (hGPCR21).
GN Name=CysLTR2; Synonyms=CysLTR2, CysLTR2R,
OC Homo sapiens (Human).
CC Bakaryot; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20374466; PubMed=10913337; DOI=10.1006/dbrc.2000.3140;
RA Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
RA Nishikawa T., Kawai Y., Masuo Y., Isega T., Suzuki Y., Sugano S.,
RA Furutachi K.;
RT "The molecular characterization and tissue distribution of the human
RT CysLein] leukotriene CysLTR2 receptor";
RL Biochem. Biophys. Res. Commun. 274:316-322(2000)
[2]
SEQUENCE FROM N.A.
RX MEDLINE=20459128; PubMed=10851239; DOI=10.1074/jbc.M003490200;
RA Helse C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
RA Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
RA Williams D.L., Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
RA Liu Y., Austen C.P., George S.R., O'Neill G.P., Metters R.M.,
RA Lynch K.R., Evans J.F.;
RT "Characterization of the human cysteinyl leukotriene 2 receptor";
RL J. Biol. Chem. 275:30531-30536(2000).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=20545741; PubMed=11093801;
RA Nockacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
RA Kivaki O.;
RT "Molecular cloning and characterization of a second human cysteinyl
RT leukotriene receptor: discovery of a subtype selective agonist";
RL Mol. Pharmacol. 58:1501-1508 (2000).
[4]
SEQUENCE FROM N.A.
RX MEDLINE=22040266; PubMed=12044878;
RA Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL FEBS Lett. 520:97-101(2002).
[5]
SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX PubMed=5057823; DOI=10.1038/nature02379;
 RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
 RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,
 RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
 RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
 RA Ashwell R.I.S., Babage A.K., Bagguley C.L., Bailey J., Banerjee R.,
 RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
 RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,
 RA Chieg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
 RA Deloukas P., Dhami P., Dunham I., Dunn M., Barthow M.E.,
 RA Ellington A.G., Faulker L., Frankish A.G., Frankland J., French L.,
 RA Garner P., Garnett J., Gilbert U.G.R., Gilson C.J., Ghori J.,
 RA Grafham D.V., Griddle S.M., Griffiths C., Hall R.E., Hammond S.,
 RA Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
 RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
 RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
 RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,
 RA Mashnezh-Mohammadi M., McLaren S.J., McMurray A., Milne S.,
 RA Moore M.J.F., Nickerson B., Porter K.M., Rice C.M., Seearle S.,
 RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Seearle S.,
 RA Sehra H.K., Showkhen R., Skuce C.D., Smith M., Steward C.A.,
 RA Sycamore N., Teeter J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
 RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
 RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
 RT "The DNA sequence and analysis of human chromosome 13."
 RL Nature 428:522-528(2004).
 RP SEQUENCE OF 17-346 FROM N.A.
 RA Suga H.;
 RT Homo sapiens cysteinyl leukotriene receptor 1 like receptor.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 mediated via a G-protein that activates a phosphatidylinositol-
 calcium second messenger system. Stimulation by BAY u9773, a
 partial agonist, induces specific contractions of pulmonary veins
 and might also have an indirect role in the relaxation of the
 pulmonary vascular endothelium. The rank order of affinities for
 the leukotrienes is LTC4 > LTD4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 heart, placenta, spleen, peripheral blood leukocytes and adrenal
 gland. In lung, expressed in the interstitial macrophages, and
 slightly in smooth muscle cells.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL, AB038269; BAB03601.1; -;
 DR EMBL, AF254664; AAG17281.1; -;
 DR EMBL, AF279611; AAK69485.1; -;
 DR EMBL, AB083603; BAB89316.1; -;
 DR EMBL, AY389504; AAO91330.1; -;
 DR EMBL, AL137118; CAC29102.1; -;
 DR EMBL, AB041644; BAB16379.1; -;
 DR Genew; HGNC:18274; CYSLTR2.
 DR MIM; 605666; -;
 DR GO; GO:0004974; F:leukotriene receptor activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR004071; CytoLeuk_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01533; CYSLTR2RCPTR.

DR PRINTS; PR00237; GPCR_RHODOPEN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; FALSE_NEG.
 DR PROSITE; PS00262; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 42
 FT TRANSMEM 43 63
 FT DOMAIN 64 72
 FT TRANSMEM 73 93
 FT DOMAIN 94 123
 FT TRANSMEM 124 144
 FT DOMAIN 145 153
 FT TRANSMEM 154 174
 FT DOMAIN 175 204
 FT TRANSMEM 205 225
 FT DOMAIN 226 245
 FT TRANSMEM 246 266
 FT DOMAIN 267 286
 FT TRANSMEM 287 307
 FT DOMAIN 308 346
 FT DISULFID 111 187
 FT CARBOHYD 20 20
 FT CARBOHYD 26 26
 FT CARBOHYD 30 30
 FT CARBOHYD 181 181
 SQ SEQUENCE 346 AA; 39635 MW; EBS4AA42DDCESEB4 CRC64;
 Query Match 100.0%; Score 1788; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1e-103;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MERKFMISLOPSSISVSEMEBNGTFSSNNNSNRCIENFKKEFFPIYVLIIFPMGVLANGLSI 60
 DB 1 MERKFMISLOPSSISVSEMEBNGTFSSNNNSNRCIENFKKEFFPIYVLIIFPMGVLANGLSI 60
 QY 61 YVFLQPYKKSTSVNFMNLAIISDLIFSTLPPRADYVIRGSNWIFGDIACRIMSISLVY 120
 DB 61 YVFLQPYKKSTSVNFMNLAIISDLIFSTLPPRADYVIRGSNWIFGDIACRIMSISLVY 120
 QY 121 NMYSTYFLTVSVRFLAMVHPFLHLHTSIRSMWICGIIWIMASSIMLLDSGSSQ 180
 DB 121 NMYSTYFLTVSVRFLAMVHPFLHLHTSIRSMWICGIIWIMASSIMLLDSGSSQ 180
 QY 181 NGSVTSCELEINLYKIAKIQTMNYIALVVGCLLPFTLSICYLLIRIVLAKVEPESGLRV 240
 DB 181 NGSVTSCELEINLYKIAKIQTMNYIALVVGCLLPFTLSICYLLIRIVLAKVEPESGLRV 240
 QY 241 SHRKALTTITITLIIIFLCFLPYHTLRVHLTTWVGLCKDRHLKALVITTLAANACF 300
 DB 241 SHRKALTTITITLIIIFLCFLPYHTLRVHLTTWVGLCKDRHLKALVITTLAANACF 300
 QY 301 NPLLYVFAGENFKDKLSLRGHOKATKCVFVSWLAKRETV 346
 DB 301 NPLLYVFAGENFKDKLSLRGHOKATKCVFVSWLAKRETV 346
 RESULT 2
 AAH69160 PRELIMINARY; PRT; 346 AA.
 AC AAH69160;
 DT 10-MAY-2004 (TREMBLrel. 27, Created)
 DT 10-MAY-2004 (TREMBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TREMBLrel. 27, Last annotation update)
 DE Cysteinyl leukotriene receptor 2.
 GN CYSLTR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_Taxid=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Synthetic constructs;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Rubin G.M., Hong L.,
 RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Caraminci P., Prange C.,
 RA Raba S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Vallaloo D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakeley A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywnicki M.I., Skalka U., Smallie D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISUE-Synthetic constructs;
 RA Scrausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC069160; AF069160.1; -
 KW Receptor.
 SQ SEQUENCE 346 AA; 39635 MW; EB54A4A2DDC5EB4 CRC64;
 Query Match 100.0%; Score 1788; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1e-103;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Ohishi T., Soga T., Matsushima H., Furuchi K.;
 RT "Characterization of the cloned rat and porcine cysleinyl leukotriene
 RT receptor";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for cysleinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol-
 CC calcium second messenger system (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AB052662; BAB60817.1; -
 DR InterPro: IPR004071; Cysleuk_Receptor.
 DR InterPro: IPR000276; GPCR_Rhodopn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01533; CYSTRRECPTR.
 DR PRINTS: PR00237; GPCRHOOPSPN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_P1.1; FALSE_NEG.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_P1.2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 43
 FT TRANSSEM 44 64
 FT DOMAIN 65 73
 FT TRANSSEM 74 94
 FT DOMAIN 95 124
 FT TRANSSEM 125 145
 FT DOMAIN 146 154
 FT TRANSSEM 155 175
 FT DOMAIN 176 205
 FT TRANSSEM 206 226
 FT DOMAIN 227 246
 FT TRANSSEM 247 267
 FT DOMAIN 268 287
 FT TRANSSEM 288 308
 FT DOMAIN 309 345
 FT DISFID 112 188
 FT CARBOHYD 20 20
 FT CARBOHYD 29 29
 FT CARBOHYD 177 177
 FT CARBOHYD 184 184
 SQ SEQUENCE 345 AA; 39410 MW; 5D1B1FB89BB95905 CRC64;
 Query Match 79.8%; Score 1427.5; DB 1; Length 345;
 Best Local Similarity 79.3%; Pred. No. 2.7e-81;
 Matches 275; Conservative 25; Mismatches 44; Indels 3; Gaps 2;

QY 300 FNFLLYYFAGENFKDLKSLARKGHPOKATKCVFVSVMLRKETRY 346
DB 301 FNFLLYYFAGENFKDLKSLARKGRQ--KTRCGFVSVMLRKETRY 345

RESULT 4
ID 08R528 PRELIMINARY; PRT; 309 AA.
AC 08R528;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Cysteiny1 leukotriene 2 receptor.
GN Name=Cyslt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013942; PubMed=11854273;
RA Ogasawara H, Ishii S., Yokomizo T., Kakinuma T., Komine M.,
RA Tamaki K., Shimizu T., Izumi T.,
RT Characterization of Mouse Cysteiny1 Leukotriene Receptors mCysLT1 and
RT mCysLT2. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES AND TISSUE
RT DISTRIBUTION.";
RL J. Biol. Chem. 277:18763-18768 (2002).
DR EMBL; AB058930; BAB86881.1; -.
DR MGD; MGI:1917336; Cyslt2.
DR GO; GO:0016020; Gmembrane; IDA.
DR GO; GO:0001631; F:cysteiny1 leukotriene receptor activity; IDA.
DR InterPro; IPR004071; Cysleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01533; CYSLTRCPTR.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.
DR KEGG; K01101; GPCR.
SQ SEQUENCE 309 AA; 35226 MW; 96FA0C6B8A96974 CRC64;

Query Match 67.3%; Score 1204; DB 2; Length 309;
Best Local Similarity 73.4%; Pred. No. 2e-67;
Matches 226; Conservative 30; Mismatches 52; Indels 0; Gaps 0;
QY 17 MEPTGTFSSNNNSRNCIENFKREPPPIVLIIFFMGVLGNGISIVVFLQPYKKSSTVNVF 76
DB 1 MEPTGTFSSNNNSRNCIENFKREPPPIVLIIFFMGVLGNGISIVVFLQCKKKSISVNVF 60
QY 77 MNLAISDDLFIETLPFRADYLRGSNMIFGDLACRIMSYSLYVNNYSSIFLTVLSVVR 136
DB 61 MNLAISDDLFIETLPFRADYLRGSNMIFGDLACRIMSYSLYVNNYSSIFLTVLSVVR 120
QY 137 FLAMHPPFLHAYTSRSAMILCGIITWILMASSIMLLDSGQNSQSVTSCLEANIYKXA 196
DB 121 FLATVHPFPMFHTSVRSAMILCGIITWILMASSIMLLDSGQNSQSVTSCLEANIYKXA 180
QY 197 KLOTMYIALVVGCLLPFTLSICYLLIRVLKIVKVEPSGRLVSHRKKALLTIITLIIF 256
DB 181 SLIIMNHIAVAGFLPFLTLTTCYLLIRILKAEIPSGPPRAHKKALLTIITLIIF 240
QY 257 FLGFLPHTLRLTVAHLLTWKVLCKDLHKLAVITTLAANAACFNPFLYYFAGENFKDL 316
DB 241 LKCFLEPYHARLTLVWPKDSGCVLHKAIVITTLMAAANSQNPFLYYFAGENFKDL 300
QY 317 KSLARKGH 324
DB 301 RAIFSKVH 308

RESULT 5
CLT2_MOUSE
ID CLT2_MOUSE STANDARD; PRT; 309 AA.
AC Q920A1;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cysteiny1 leukotriene receptor 2 (CysLT2).
GN Name=Cyslt2; Synonyms=Cyslt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=2161669; PubMed=11591709; DOI=10.1074/jbc.M107556200;
RA Hui Y., Yang G., Galczenski H., Figueroa D.J., Austin C.P.,
RA Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.,
RT "The murine cysteiny1 leukotriene 2 (CysLT2) receptor. cDNA and
RT genomic cloning, alternative splicing, and in vitro
RT characterization.";
RL J. Biol. Chem. 276:47489-47495 (2001).
CC -1- FUNCTION: Receptor for cysteiny1 leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system. The rank order of affinities for
CC the leukotrienes is LTC4 = LTD4 >> LTE4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed at low levels, with highest
CC expression in the spleen, thymus and adrenal gland, and lower in
CC the kidney, brain and peripheral blood leukocytes.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AF31658; MAK97354.1; -.
DR MGD; MGI:1917336; Cyslt2.
DR GO; GO:0016020; Gmembrane; IDA.
DR GO; GO:0001631; F:cysteiny1 leukotriene receptor activity; IDA.
DR InterPro; IPR004071; Cysleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01533; CYSLTRCPTR.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS50237; G_PROTEIN_RECPR_F1_1; FALSE_NEG.
DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 26
FT TRANSMEM 27 47
FT DOMAIN 48 56
FT TRANSMEM 57 77
FT DOMAIN 78 98
FT TRANSMEM 99 119
FT DOMAIN 120 138
FT TRANSMEM 139 159
FT DOMAIN 160 187
FT TRANSMEM 188 208
FT DOMAIN 209 229
FT TRANSMEM 230 250
FT DOMAIN 251 271
FT TRANSMEM 272 292
FT DOMAIN 293 309
FT DISULFID 95 171
FT CARBOHYD 14 14
SQ SEQUENCE 309 AA; 35227 MW; 327B1A46BDD2A02 CRC64;

Query Match 66.9%; Score 1197; DB 1; Length 309;
Best Local Similarity 72.7%; Pred. No. 5.4e-67;
Matches 224; Conservative 31; Mismatches 53; Indels 0; Gaps 0;
QY 17 MEPTGTFSSNNNSRNCIENFKREPPPIVLIIFFMGVLGNGISIVVFLQPYKKSSTVNVF 76

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DB 1 MEVGTGSSYSNRKCTIENFKREFFPIVLIIFPMGALNGPSIYVFLQTKKSTSVNF 60
QY 77 MLNLAIISDLFIPTLPFRADYVIRGSMNIFGDLACRIMSYSLVNMYSIYFLTVLSVVR 136
DB 61 MLNLATSDFLPISITLPRADYVIRGSMNIFGDLACRIMSYSLVNMYSIYFLTVLSVVR 120
QY 137 FLAMVHPRLHNTSIRSAWILGIIWILMASSIMLDSSEONGSTSCLELNKYIA 196
DB 121 FOATVHPRMFHVSVRSAMWILGIIWVFMASALLVNGQEKDNIISCLELSPKFK 180
QY 197 KLOTNMYIALVAGCLLPFTLSICYLIIIRVLKVEPESGLRVSHRKALTTIITLIIIF 256
DB 181 SLILNMHIAVAGCLLPFTLTTCYLLIIRILKREIPESGPRAAHRAALTTIIVIAMTF 240
QY 257 FLCELPYHTLRTVHLTWKVGCLCKDRHLKALVITLAAANACFNPLLYPAGENPKDR 316
DB 241 LICEPLPHALRTLHLVTDKSCDVLHKAIVITLMAANSCEFNPFLYPAGENPKARL 300
QY 317 KSALRKGH 324
DB 301 RALFSKVH 308

RESULT 6
CLUT2_RAT STANDARD; PRT; 309 AA.
AC 0924TG;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyll leukotriene receptor 2 (CysLTR2) (R5BP132).
GN Name=CysLTR2; Synonym=CysLT2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Ohishi T., Soga T., Matsushime H., Furuchi K.;
RT "Characterization of the cloned rat and porcine cysteinyl leukotriene
RT receptor."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AB052661; BAB60816.1; -.
DR RGD; 619797; Cyslt2.
DR InterPro; IPR004071; Cysleuk_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1533; CYSLRECEPT.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 26 Extracellular (Potential).
FT TRANSMEM 27 47 1 (Potential).
FT DOMAIN 48 56 Cytoplasmic (Potential).
FT TRANSMEM 57 77 2 (Potential).
FT DOMAIN 78 98 Extracellular (Potential).

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FT TRANSMEM 99 119 3 (Potential).
FT DOMAIN 120 137 Cytoplasmic (Potential).
FT TRANSMEM 138 158 4 (Potential).
FT DOMAIN 159 187 Extracellular (Potential).
FT TRANSMEM 188 208 5 (Potential).
FT DOMAIN 209 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT DOMAIN 293 309 Cytoplasmic (Potential).
FT DISULFID 95 171 By similarity.
FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 167 167 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;

Query Match 66.4%; Score 1187; DB 1; Length 309;
Best Local Similarity 73.1%; Pred. No. 2,3e-66;
Matches 225; Conservative 26; Mismatches 57; Indels 0; Gaps 0;

QY 17 MEVGTGSSYSNRKCTIENFKREFFPIVLIIFPMGALNGPSIYVFLQTKKSTSVNF 76
DB 1 MGVTGTPSYSDKRCCTIENFKRDFPIVLIIFPMGALNGPSIYVFLQTKKSTSVNF 60
QY 77 MLNLAIISDLFIPTLPFRADYVIRGSMNIFGDLACRIMSYSLVNMYSIYFLTVLSVVR 136
DB 61 MLNLATSDFLPISITLPRADYVIRGSMNIFGDLACRIMSYSLVNMYSIYFLTVLSVVR 120
QY 137 FLAMVHPRLHNTSIRSAWILGIIWILMASSIMLDSSEONGSTSCLELNKYIA 196
DB 121 FLATAPHPFOMLHTSVRSAMWILGIIWVFMASGGLLKHGQKKNNTTICFELNLQKFX 180
QY 197 KLOTNMYIALVAGCLLPFTLSICYLIIIRVLKVEPESGLRVSHRKALTTIITLIIIF 256
DB 181 NLVLIANYIALVAGVFLPFTLTTCYLLIIRILKREIPESGPRDAQKALTTIIVIAMTF 240
QY 257 FLCELPYHTLRTVHLTWKVGCLCKDRHLKALVITLAAANACFNPLLYPAGENPKDR 316
DB 241 LICEPLPHALRTLHLVTDKSCDVLHKAIVITLMAANSCEFNPFLYPAGENPKARL 300
QY 317 KSALRKGH 324
DB 301 RALFSKVH 308

RESULT 7
CLUT1_RAT STANDARD; PRT; 339 AA.
AC 0924TG;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyll leukotriene receptor 1 (CysLTR1).
GN Name=CysLTR1; Synonym=CysLT1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA Ohishi T., Soga T., Matsushime H., Furuchi K.;
RT "Characterization of cloned rat and porcine cysteinyl leukotriene
RT receptor."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC constriction of the microvascular smooth muscle during an
CC inflammatory response. This response is mediated via a G-protein
CC that activates a phosphatidylinositol-calcium second messenger
CC system (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----

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CC -----

DR EMBL; AB052685; BAB60825.1; -

DR RGD; 619796; Cysleu1.

DR InterPro; IPR004071; Cysleuk_receptor.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR01533; CYSLTRRECPTR.

DR PROSITE; PS00237; GPCRHOODPSN.

DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_1; FALSE_NEG.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 30 1 (Potential).

FT TRANSMEM 52 59 2 (Potential).

FT TRANSMEM 60 80 2 (Potential).

FT TRANSMEM 81 108 3 (Potential).

FT TRANSMEM 109 129 3 (Potential).

FT TRANSMEM 130 143 4 (Potential).

FT TRANSMEM 144 164 5 (Potential).

FT TRANSMEM 165 195 5 (Potential).

FT TRANSMEM 196 216 6 (Potential).

FT TRANSMEM 217 232 6 (Potential).

FT TRANSMEM 233 253 7 (Potential).

FT TRANSMEM 254 278 7 (Potential).

FT TRANSMEM 279 299 7 (Potential).

FT TRANSMEM 300 339 7 (Potential).

FT DISULFID 98 175 1 (Potential).

FT CARBOHYD 6 6 1 (Potential).

FT CARBOHYD 171 171 1 (Potential).

FT CARBOHYD 171 171 1 (Potential).

SQ SEQUENCE 339 AA; 39143 MW; 281941DF050DF8BA CRC64;

Query Match 31.7%; Score 567.5; DB 1; Length 339;

Best Local Similarity 36.7%; Pred. No. 8.6e-28;

Matches 122; Conservative 70; Mismatches 115; Indels 25; Gaps 8;

22 TFSNNRNCTIENFKRPPPIVYLIFFWGANGLSIVFLQPKKSTSVNFMNLTAIS 81

10 SFSNNRNCHD-TIDEFRNQVSTVMSIVGFGNSFVLVLTIKYHESAPQVYMINLA 68

82 ISLLFTSTLPFADYTLRGSNMFQGLACRINSYSLYNMSSIFLYLVSVRFLAMV 141

69 IADLCVCTLPFLRVVYVHKGWFFGDFLCRLTYVALYVNLXCSIFPMTAMSPFRCAIV 128

142 HPEPLAHVTSIRSAMWILCGIWI-LIMASSIMLDGSGSEONGSVTSCLEINLYKIAK-L 198

129 FPYQNNINLVYQKARVCVGIWIFVLTSSPFLSSSYDEKNNKTCFEPDOKQTKKV 188

199 QTMNNTALVVGCLLPFTLSICVLLIRVLKVEVESGRLVSHRKALTTIITLIIFPL 258

189 LVLYAVSLIFGFIPIVTVIIVCYTMILITLKNYMKKN-LPERRAKAIGMIIVTAAPLV 246

259 CILPHTLTATVH--TTWKVGLCKD--RLHKALVITLALAAANACPNLLTYAGNED 314

247 SFMPYHIQRAIHHLHFLHSFRSCDVLIRQKSVVITLSLAASCCPDLIPFSGGNFR 306

315 RLKSAALRK-----GHPQAKATKC 332

307 RL-STFRKGSLSGMTYIPKKKASLPKGEEMC 337

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cysteinyll leukotriene receptor 1 (CysLTR1).

GN Name=CysLTR1; Synonyms=CysLTR1;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

NCBI_TaxID=9823;

RNA [1]

RP SEQUENCE FROM N.A.

RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,

RA Ohishi T., Soga T., Matsushima H., Furuichi K.;

RT "Characterization of cloned rat and porcine cysteinyl leukotriene

RT receptors."

RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.

CC -!- FUNCTION: Receptor for cysteinyl leukotrienes mediating

CC contraction of the microvascular smooth muscle during an

CC inflammatory response. This response is mediated via a G-protein

CC that activates a phosphatidylinositol-calcium second messenger

CC system (By similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----

DR EMBL; AB052686; BAB60826.1; -

DR InterPro; IPR004071; Cysleuk_receptor.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR01533; CYSLTRRECPTR.

DR PROSITE; PS00237; GPCRHOODPSN.

DR PROSITE; PS00237; G_PROTEIN_RECPR_F1_1; FALSE_NEG.

DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 31 1 (Potential).

FT TRANSMEM 52 59 2 (Potential).

FT TRANSMEM 60 80 2 (Potential).

FT TRANSMEM 81 108 3 (Potential).

FT TRANSMEM 109 129 3 (Potential).

FT TRANSMEM 130 143 4 (Potential).

FT TRANSMEM 144 164 5 (Potential).

FT TRANSMEM 165 195 5 (Potential).

FT TRANSMEM 196 216 6 (Potential).

FT TRANSMEM 217 232 6 (Potential).

FT TRANSMEM 233 253 7 (Potential).

FT TRANSMEM 254 278 7 (Potential).

FT TRANSMEM 279 299 7 (Potential).

FT TRANSMEM 300 339 7 (Potential).

FT DISULFID 99 176 1 (Potential).

FT CARBOHYD 6 6 1 (Potential).

FT CARBOHYD 18 18 1 (Potential).

FT CARBOHYD 172 172 1 (Potential).

FT CARBOHYD 265 265 1 (Potential).

FT CARBOHYD 265 265 1 (Potential).

SQ SEQUENCE 340 AA; 38986 MW; 54P9372A121CB413 CRC64;

Query Match 31.5%; Score 563; DB 1; Length 340;

Best Local Similarity 37.4%; Pred. No. 1.6e-27;

Matches 116; Conservative 75; Mismatches 101; Indels 18; Gaps 6;

24 SNNNSRNCTIENFKRPPPIVYLIFFWGANGLSIVFLQPKKSTSVNFMNLTAIS 83

12 ASSNTCDTIIDDFRQVSTVMSIVGFGNSFVLVLTIKYHESAPQVYMINLA 71

84 DILFTSTLPFADYTLRGSNMFQGLACRINSYSLYNMSSIFLYLVSVRFLAMHP 143

72 DILCVCTLPFLRVVYVHKGWFFGDFLCRLSTYVALYVNLXCSIFPMTAMSPFRCAIV 131

Db

Qy

Db

Qy

Db

Qy

Db

Qy

OY 144 FRLHWTNSIRSAWILGCIWI-LIMASSIMLDGSGEONSQSVTSCLELNIYKIAK--LQT 200
 DB 132 VONINLTHKKAKVCAIWMFVLITSPFMSTSYDEKKNVTCPEPOXNOKYHVLV 191
 OY 201 MNYIALVVGCLLPFTLSICYLILIRVLLKVEVPSGSRVSHRKAITIIITLIFELCF 260
 DB 192 LHVSLVGVFIPIVIIIVCTMIILTLKNSMKKN--ISRRKKAIGMIIVTAAFLISF 249
 OY 261 LPHYTLATVHLTTKVGGLCD-----RLKALVITLALAAANACPNLLYFAGENF 312
 DB 250 MPYHIOPTIHLHF-----LHNDTKHCDVLRMOKSVXITLSIAASNCCEFDPLYPFGSGNF 305
 OY 313 KDRLSALRK 322
 DB 306 REGI-STFRK 314
 RESULT 9
 CLTI_MOUSE STANDARD; PRT; 352 AA.
 AC Q99JA4; Q9J071; Q9UK47;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cysteiny1 leukotriene receptor 1 (CysLTR1) (Cysteiny1 leukotriene D4 receptor) (LTD4 receptor)
 GN Name=CysLTR1; Synonym=CysLT1, CysLTR;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=129/SV;
 RX PubMed=1126226; DOI=10.1073/pnas.041624398;
 RA Mekawa A., Kanoka Y., Lam B.K., Austen K.F.;
 RT "Identification in mice of two isoforms of the cysteiny1 leukotriene 1
 RT receptor that result from alternative splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12256-12261(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6; TISSUE=Trachea;
 RX MEDLINE=1552333; PubMed=11705457; DOI=10.1016/S0006-2952(01)00774-2;
 RA Martin V., Sawyer N., Stocco R., Unect D., Letner M.R., Abramovitz M.,
 RA Funk C.D.;
 RT "Molecular cloning and functional characterization of murine
 RT cysteiny1-leukotriene 1 (CysLTR1) receptors."
 RL Biochem. Pharmacol. 62:1193-1200(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=2124038; PubMed=11342226; DOI=10.1016/S0167-4781(00)00271-2;
 RA Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann E.K.;
 RT "Identification of a murine cysteiny1 leukotriene receptor by
 RT expression in Xenopus laevis oocytes."
 RL Biochim. Biophys. Acta 1517:455-459(2001).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=T-cell;
 RA Ogasawara H., Izumi T., Shimizu T.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueller K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diacumbo L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Slaughter M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshikiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smallue D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for cysteiny1 leukotrienes mediating
 CC constriction of the microvascular smooth muscle during an
 CC inflammatory response. This response is mediated via a G-protein
 CC that activates a phosphatidylinositol-calcium second messenger
 CC system. The rank order of affinities for the leukotrienes is LTD4
 CC >> LTE4 = LTC4 >> LTB4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=Q99JA4-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=Q99JA4-2; Sequence=VSP_001921.
 CC -1- TISSUE SPECIFICITY: Widely expressed, with higher expression in
 CC the lung and skin, intermediate levels in the heart, kidney and
 CC stomach and lower levels in several other tissues. Isoform 1 is
 CC the most abundant form in all tested tissues.
 CC -1- MISCELLANEOUS: MK-571, a selective antagonist, was shown to
 CC inhibit eosinophilia, bronchial hyperreactivity and microvascular
 CC leakage. Zafirlukast (Accolate) and pranlukast (Onon) were also
 CC shown to be selective antagonists.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF329272; AAK16715.1; -;
 CC EMBL; AF329272; AAK16716.1; -;
 CC EMBL; AF205830; AAK15433.1; -;
 CC EMBL; AF263370; AAF73047.1; -;
 CC EMBL; AB044087; BAA96809.1; -;
 CC EMBL; BC027102; AAH27102.1; -;
 CC HSP; F34996; 1DD.
 CC MGD; MG1:1926218; CysLTR1.
 CC GO; GO:0005887; C:integral to plasma membrane; IDA.
 CC GO; GO:0004974; F:leukotriene receptor activity; IDA.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . . IDA.
 CC InterPro; IPR004071; CysLeuk_receptor.
 CC InterPro; IPR000276; GPCR_KnoDpsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR01533; CYSLTRPCPTR.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NGS.
 CC PROSITE; PS02652; G_PROTEIN_RECP_F1_2; 1.
 CC Alternative splicing; G-protein coupled receptor; Glycoprotein;
 CC Transmembrane.
 CC DOMAIN 1 43
 CC FT DOMAIN 1 43
 CC FT TRANSMEM 44 64
 CC FT DOMAIN 65 72
 CC FT TRANSMEM 73 93
 CC FT DOMAIN 94 121
 CC FT TRANSMEM 122 142
 CC FT DOMAIN 143 156
 CC FT TRANSMEM 157 177
 CC FT DOMAIN 178 208
 CC FT TRANSMEM 209 229
 CC
 CC Extracellular (Potential).
 CC 1 (Potential).
 CC Cytoplasmic (Potential).
 CC 2 (Potential).
 CC Extracellular (Potential).
 CC Extracellular (Potential).
 CC Cytoplasmic (Potential).
 CC 4 (Potential).
 CC Extracellular (Potential).
 CC 5 (Potential).

FT	DOMAIN	230	245	Cytoplasmic (Potential).
FT	TRANSMEM	246	266	6 (Potential).
FT	DOMAIN	267	291	Extracellular (Potential).
FT	TRANSMEM	292	312	7 (Potential).
FT	DOMAIN	313	352	Cytoplasmic (Potential).
FT	DISULFID	111	188	By similarity.
FT	CARBOHYD	15	15	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	19	19	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	26	26	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	184	184	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	1	13	Missing (in isoform 2).
FT				/FTId=VSP_001921.
FT	CONFLICT	176	176	Y -> D (in Ref. 3).
FT	SEQ	352 AA;	40715 MW;	SBDCC94B3F1CDDCAB CRC64;
Query Match		31.3%;	Score 560;	DB 1; Length 352;
Beet Local Similarity		38.5%;	Pred. No. 2.6e-27;	
Matches	117;	Conservative	69;	Mismatches 108; Indels 10; Gaps 6;
QY	26	NNSRACITENFGRKEFFPIYLIIIFMGVIGNELSIVFLOPKKSTVNVFPLNLAISDL	85	
DB	26	NNTCHDITIDEPNGQVSTMTSVISVGFPGNSFVLIVLKITKHEKSAQVYMINALIDL	85	
QY	86	LFISTLPPRADYYLRGNSWIFGDLACRIMSYSLVYNYMTSSIVFTLVSVREFLAVHDFR	145	
DB	86	LCVCTPLPRVYVYHKKMKLFGDFLCRLTTYALYNLCSIFPMTAMSFRCVAIVFPVQ	145	
QY	146	LLHVTISISAWTLGCIWT-LIMASSIMLLDGSQNSVNSCELNLYKIAK--LQTMN	202	
DB	146	NINLTQKKARVCCGIMVFLYVLTSSPFLMTKSYDEKQNTKCFEPPONNOKKTVLLH	205	
QY	203	YIALVVGCLPEPFTLSICYLLIIRVLKVEVPEGSLRVSHRKALTTIIITLIIFPLCFLP	262	
DB	206	YVSLPEFGPIIPVTVIIVCYTMIITLLKNTMKGN--MPSRRKALGMIIVVAAFLVSPMP	263	
QY	263	YHTLTPTVLLTWM--KVGICKD--RLHKLAVITLLAANAACNPILYYFAGENFCDRLKS	318	
DB	264	YHIOCTIHLHLHSETRPCDSVLRQKSVITLLSLAASNCDFPLLYPFGSGNFRRL-S	322	
QY	319	ALRK	322	
DB	323	TPRK	326	
RESULT 10				
ID	BAC28308	PRELIMINARY;	PRT;	352 AA.
AC	BAC28308;			
DT	14-APR-2004 (Tremblrel. 27, Created)			
DT	14-APR-2004 (Tremblrel. 27, Last sequence update)			
DT	14-APR-2004 (Tremblrel. 27, Last annotation update)			
DE	Adult male colon cDNA, RIKEN full-length enriched library,			
DE	clone:0030217A18 product:CYSTB1N1YL LUKOKTR1ENE 1 RECEPTOR LONG			
OS	ISOFORM, full insert sequence.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Colon;			
RX	MEDLINE=22354683; PubMed=12466651;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Colon;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection."			

RL	Nature	409:685-690(2001).
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Colon;	
RX	MEDLINE=99279253; PubMed=10349636;	
RA	Carninci P., Hayashizaki Y. ;	
RT	"High-efficiency full-length cDNA cloning."	
RL	Meth. Enzymol. 303:19-44(1999).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Colon;	
RX	MEDLINE=20499374; PubMed=11042159;	
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,	
RT	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y. ;	
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."	
RN	Genome Res. 10:1617-1630(2000).	
RM	[5]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Colon;	
RX	MEDLINE=20530913; PubMed=11076861;	
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,	
RA	Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,	
RA	Sun H., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasbiwagi K.,	
RA	Fujimake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,	
RA	Oyoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawaji J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y. ;	
RT	"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."	
RL	Genome Res. 10:1757-1771(2000).	
RN	[6]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Colon;	
RA	Adechi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	
RA	Fukuda S., Furuno K., Hanagaki T., Hara A., Hashizume W.,	
RA	Hayaashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,	
RA	Hoti F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kaubawa T.,	
RA	Katoh H., Kawai J., Koima Y., Kondo S., Kono H., Kouma M., Koya S.,	
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,	
RA	Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,	
RA	Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,	
RA	Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,	
RA	Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,	
RA	Togami A., Toya T., Yasuniishi A., Muramatsu M., Hayashizaki Y. ;	
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AK033476; BAC28308.1; -	
KW	Receptor	
SO	SEQUENCE	352 AA; 40715 MW; 5BDC94B3F1CD0CAB CRC64;
D1	Query Match	31.3%; Score 560; DB 2; Length 352;
D2	Best Local Similarity	38.5%; Pred. No. 2.6e-27;
D3	Matches 117; Conservative 69; Mismatches 108; Indels 10; Gaps 6	
D4		
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D99		
D100		

QY 319 ALRK 322
DB 323 TFRK 326

RESULT 11
CLUT_HUMAN STANDARD, PRT, 337 AA.
ID CLUT_HUMAN
AC Q9Y271;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cysteineyl leukotriene receptor 1 (CysLTR1) (Cysteineyl leukotriene D4 receptor) (LTD4 receptor) (HG55) (HMTF81).
GN Name=CysLTR1; Synonyms=CysLT1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99318129; PubMed=10391245;
RA Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Welters K.M., Colombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.M., Bal C., Austen C.P., Chateaufort A., Stocco R., Greig G.M., Kargman S., Hooks S.B., Hosfield E., Williams D.L., Jr., Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;
RT "Characterization of the human cysteinyl leukotriene CysLTR1 receptor.";
RL Nature 399:789-793(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte, peripheral blood monocytes, and spleen;
RX MEDLINE=99393629; PubMed=10462554;
RA Sarau H.M., Ames R.S., Chambers J., Ellis C., Elshoutbagy N., Herlihy J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdoch P.R., Herlihy N.C., Halsey W., Satche G., Muir A.T., Nutallagan P., Dyck G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P.;
RT "Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor.";
RL Mol. Pharmacol. 56:657-663(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction regulated by the G-protein coupled receptor (GPCR) family.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating bronchoconstriction of individuals with and without asthma.
CC Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, edema, eosinophil migration and damage to the muscle layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4 > LTD4 = LTD4 > LTD4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in spleen and peripheral blood leukocytes. Lower expression in several tissues, such as lung (mostly in smooth muscle bundles and alveolar macrophages), placenta, small intestine, pancreas, colon and heart.
CC -1- MISCELLANEOUS: Selective antagonists, such as montelukast (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are used in the treatment of the asthma crisis.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; AF119711; AAD42285.1; -
CC EMBL; AF133266; AAD42778.1; -
CC EMBL; AY242130; AAO22297.1; -
CC HSSP; P34996; 1DD. CysLTR1.
CC Genew; HGNC:17451; CysLTR1.
CC MIM; 30201; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005624; C: membrane fraction; TAS.
CC GO; GO:0004974; P: leukotriene receptor activity; TAS.
CC GO; GO:0007204; P: pyrolytic calcium ion concentration elevation; TAS.
CC GO; GO:0006952; P: defense response; TAS.
CC InterPro; IPR004071; CysLeuk_receptor.
CC InterPro; IPR00276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR01533; CysLTR1.
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Transmembrane.
CC DOMAIN 1 28
FT TRANSMEM 29 49
FT DOMAIN 50 57
FT TRANSMEM 58 78
FT DOMAIN 79 106
FT TRANSMEM 107 127
FT DOMAIN 128 141
FT TRANSMEM 142 162
FT DOMAIN 163 193
FT TRANSMEM 194 214
FT DOMAIN 215 230
FT TRANSMEM 231 251
FT DOMAIN 252 276
FT TRANSMEM 277 297
FT DOMAIN 298 337
FT DISULFID 96 173
FT CARBOHYD 6 6
FT CARBOHYD 169 169
FT CARBOHYD 180 180
FT CARBOHYD 262 262
SQ SEQUENCE 337 AA; 38541 MW; B9B53940F895F245 CRC64;
Query Match 31.3%; Score 559; DB 1; Length 337;
Best Local Similarity 38.0%; Pred. No. 2,9e-27;
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;
QY 27 NSRNC--TINPKRPPPIVYLIIFKVGILGSLIVFLQPKYKSTSVNFMNLALISD 84
DB 10 SSATCHTIDIDFNRQVSTLYSMISVGFPGNPFVLYLTKTHKSAFOVYMINLAVAD 69
QY 85 LFLPSTLPFADYVYLGNSWIFGDLACRIMSYSLVYVMSYIFLTVLSVRFAMVHP 144
DB 70 LFLCVTLPLRVYVYVHKGIWLPDFLCRSTVLYLVNLSIFPMAMSFPFCIAVFPV 129
QY 145 RLHVTSIRSAWITIGIWI-LIMASIMLDGSEONGSVTSCLEMLYKIAK--LQTM 201
DB 130 QNINLVQKARVCAGIWFVILTSFPLMARPDQDKNNTCPEDPNQKNHVLVL 189
QY 202 NYALVGVCLPPFTSICVLLIIRVLKVEPSGLRSHKALTTIITLIFPLCF 261
DB 190 HYSVLPVGFPIIPVIVICVTMIITLLKSMKN--LSHKRAIGIIVVTAFLVSFM 247
QY 262 PYHTLRVHVTW--KVGCKD--RLHKALVITLALAAACNPPLYPAGNPFORLK 317
DB 248 PYHQRTHHPLHNETKPCDSVLRMOKSVVITLSLAASNCFDPLLYPSGGNFRKL- 306
QY 318 SALRK 322
DB 307 TFRK 311

Query Match	Best Local Similarity	Matches	Score	DB	Length
Query 30	NCTIEN--PKREFFPIVYLLIFPMGVLCNG--LSITYP-LDPYKKSYSVNVPMNLAI	84	27.3%;	34.9%;	23;
Db 23	NCTDENBPLKMHVLPVYIGLIFLFGPPNAVAVISTYIFPKMPKMSST--TIMNLACTD	79	64;	114;	Indels 29; Gaps 10;
Query 85	LLFFSTLPFRADYVLRGSMWIFGDLACRIMSYSLVYVMSISYFELTVLSVRFAMVHP	144			
Db 80	LLVYTSLPFLHYVASGENWIFGDPMPCKFIKFSHPNLYSIILLTCSIRRYCVIIHPM	139			
Query 145	RLHVTISRSMILGIIWILIMASSI--MLDGSSEFQNS---VTSCLNMLYKIAK	197			
Db 140	SCSFIHKTRCACVAVCAVWMIISLVAVIPMFELISTRTKRNISACIDLTSDELNTIK--	196			
Query 198	LQTMNVALVAVGCLLPFTLSICVLLIIRVLLAKVEPSGKRVSHRKLTTIIITLIIFF	257			
Db 197	--WYNLLIATATTCPLPLVYIVLCTYIIHITLHGLQDSCSK--QKARLLTILLALAY	251			
Query 258	LCGLPYHTLRTVHLTTWKVGL---CKDLRKALVYITLALANACFNPFLYYFAGENFKD	314			
Db 252	VCFPLPFLILRVIRIRIESRLISCSIBNDIHBAIVYSRPLALNFGNLLLVVVSDDNQ	311			
Query 315	RUKSALR---KGHPQAK 329				
Db 312	AVGSTVRCVSGNLEQAK 329				

ID	GP17_HUMAN	STANDARD;	PRT;	367 AA.
AC	Q13304;Q9UND6; Q9UBE21.			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Probable P2Y purinoceptor GPR17 (P2Y-1-like receptor) (R12).			
GN	Name=GPR17;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
OX	1			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=96145150; PubMed=8558062;			
RA	Report C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,			
RA	Godtula R., Gray P.W.;			
RT	"New members of the chemokine receptor gene family.";			
RL	J. Leukoc. Biol. 59:18-23(1996).			
RL	12			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Hippocampus;			
RX	MEDLINE=98181695; PubMed=9523551;			
RA	Blaesius R.H., Weber R.G., Licher P., Ogilvie A.;			
RT	"A novel orphan G protein-coupled receptor primarily expressed in the			
RT	brain is localized on human chromosomal band 2q21.";			
RL	J. Neurochem. 70:1357-1365(1998).			
CC	-1- PUNCTION: Putative receptor for putines coupled to G-proteins (By			
CC	similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	Isoid=Q13304-1; Sequence=Displayed;			
CC	Name=2;			
CC	Isoid=Q13304-2; Sequence=VSP_001987;			
CC	-1- TISSUE SPECIFICITY: Primarily expressed in brain.			
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.ftp-sib.ch/announce/			
CC	or send an email to license@ftp-sib.ch).			
CC	-----			
DR	EMBL, U33447; AAB16746.1; -			
DR	EMBL, Y12546; CAJ73144.1; -			
DR	EMBL, Z94154; CAB08107.1; -			
DR	EMBL, Z94155; CAB08108.1; -			
DR	HSPB, P34996; IIDD.			
DR	Genew; HGNC:4471; GPR17.			
DR	MTM, 603071; -			
DR	GO; GO:0005887; C:integral to plasma membrane; TM.			
DR	GO; GO:0004950; F:chemokine receptor activity; TAS.			
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. - ; TAS.			
DR	InterPro: IPR000276; GPCR Rhodops.			
DR	InterPro: IPR002286; P2_purinoceptor.			
DR	Pfam: P00001; 7tm.1; 1			
DR	PRINTS, PR00237; GPCRKHODPSN.			
DR	PROSITE, PS00237; G_PROTEIN_RECP_F1_1; 1.			
DR	PROSITE, PS00267; G_PROTEIN_RECP_F2_1; 1.			
KM	Alternative splicing; G-protein coupled receptor; Glycoprotein;			
KM	Transmembrane.			
FT	DOMAIN 1 64	Extracellular (Potential).		
FT	TRANSEM 65 85	1 (Potential)		
FT	DOMAIN 86 92	Cytoplasmic (Potential).		
FT	TRANSEM 93 113	2 (Potential)		
FT	DOMAIN 114 133	Extracellular (Potential).		

FT	TRANSMEM	134	154	175	3 (Potential)	Cytoplasmic (Potential)
FT <th>TRANSMEM</th> <th>134</th> <th>154</th> <th>175</th> <th>3 (Potential)</th> <th>Cytoplasmic (Potential)</th>	TRANSMEM	134	154	175	3 (Potential)	Cytoplasmic (Potential)
FT <th>TRANSMEM</th> <th>176</th> <th>196</th> <th>196</th> <th>4 (Potential)</th> <th>Extracellular (Potential)</th>	TRANSMEM	176	196	196	4 (Potential)	Extracellular (Potential)
FT <th>TRANSMEM</th> <th>197</th> <th>223</th> <th>223</th> <th>5 (Potential)</th> <th>Extracellular (Potential)</th>	TRANSMEM	197	223	223	5 (Potential)	Extracellular (Potential)
FT <th>TRANSMEM</th> <th>224</th> <th>244</th> <th>244</th> <th>5 (Potential)</th> <th>Cytoplasmic (Potential)</th>	TRANSMEM	224	244	244	5 (Potential)	Cytoplasmic (Potential)
FT <th>TRANSMEM</th> <th>245</th> <th>260</th> <th>260</th> <th>6 (Potential)</th> <th>Extracellular (Potential)</th>	TRANSMEM	245	260	260	6 (Potential)	Extracellular (Potential)
FT <th>TRANSMEM</th> <th>261</th> <th>281</th> <th>281</th> <th>7 (Potential)</th> <th>Cytoplasmic (Potential)</th>	TRANSMEM	261	281	281	7 (Potential)	Cytoplasmic (Potential)
FT <th>TRANSMEM</th> <th>282</th> <th>308</th> <th>329</th> <th>7 (Potential)</th> <th>Cytoplasmic (Potential)</th>	TRANSMEM	282	308	329	7 (Potential)	Cytoplasmic (Potential)
FT <th>TRANSMEM</th> <th>309</th> <th>329</th> <th>367</th> <th>By similarity</th> <th>Cytoplasmic (Potential)</th>	TRANSMEM	309	329	367	By similarity	Cytoplasmic (Potential)
FT <th>DISULFID</th> <th>132</th> <th>209</th> <th>42</th> <th>N-linked (GlcNAc . . .)</th> <th>(Potential)</th>	DISULFID	132	209	42	N-linked (GlcNAc . . .)	(Potential)
FT <th>CARBOHYD</th> <th>142</th> <th>204</th> <th>204</th> <th>N-linked (GlcNAc . . .)</th> <th>(Potential)</th>	CARBOHYD	142	204	204	N-linked (GlcNAc . . .)	(Potential)
FT <th>CARBOHYD</th> <th>204</th> <th>282</th> <th>282</th> <th>N-linked (GlcNAc . . .)</th> <th>(Potential)</th>	CARBOHYD	204	282	282	N-linked (GlcNAc . . .)	(Potential)
FT <th>VANSPIC</th> <th>1</th> <th>28</th> <th>28</th> <th>Missing (in isoform 2)</th> <th>(Potential)</th>	VANSPIC	1	28	28	Missing (in isoform 2)	(Potential)
FT <th>SEQUENCE</th> <th>367 AA</th> <th>40989 MW</th> <th>133FBE97BB83C60C CRC64</th> <th>/FTID=VSP 001987</th> <th></th>	SEQUENCE	367 AA	40989 MW	133FBE97BB83C60C CRC64	/FTID=VSP 001987	
SO <th>Query Match</th> <th>27.1%</th> <th>Score 484.5</th> <th>DB 1</th> <th>Length 367</th> <th></th>	Query Match	27.1%	Score 484.5	DB 1	Length 367	
SO <th>Beet Local Similarity</th> <th>34.4%</th> <th>Pred. No. 1.3e-22</th> <th></th> <th></th> <th></th>	Beet Local Similarity	34.4%	Pred. No. 1.3e-22			
SO <th>Matches 116</th> <th>Conservative 65</th> <th>Mismatches 131</th> <th>Indels 25</th> <th>Gaps 10</th> <th></th>	Matches 116	Conservative 65	Mismatches 131	Indels 25	Gaps 10	
QY	11	SISVSEMPNG--TFSNNSNHCITEN-FKKEPPIYLLIFFWGLNGLSIVFP	66			
DB	28	SMNGEJVAPEGLITITFSLATEQCQCFRPLEMFLFASLYLDLFIATLVGNTALMLFIRD	87			
QY	67	YKKSIVAVFMLNLAIIDLFIPTLPFRADYYLRGSMNIFGDLAGRISYSLYNNYSSI	126			
DB	88	HKSQTPAVVFLMHLAVADLSCVLVPRTLVPYHPSGNHMPFGBIACRLNGFLYNNYASI	147			
QY	127	YELTAVLVPRPLAMHPRLHVTISIRAMILCGIIMLLI-MASSIMLDSSEBNGSVT	185			
DB	148	YFLTISADRFALVHPVKSLELRPLVYAHNLACFLMWVAVANAPLLVSPQIVQTHNTV	207			
QY	186	SCLEMLKRIAKLQTMNYIALVVGCLPPEFTLICYLLIRVLKVEVPESGLRVSHR--	243			
DB	208	VCLQ--LVR-EKASHNALVSLAVATPFPITVTCYLLISL-----RQGLRVEKYLK	258			
QY	244	-KALTITITITLIFLFCPLPYHTLTVMKTV--GLCKORLNRALV--ITLALAANA	298			
DB	259	TKAVVMIAIVLAIPLVCFVPHVYVNSVYVLAHRSAGASCAPQRIALANRITSCLTSLNG	318			
QY	299	CENPLLYFAGENFKDLKSL---RGHPQKATK	331			
DB	319	ALDPIYFFVAKEFRHNLGNLCKRLKGPPEPSFGK	355			
RESULT 15						
Q8NS57						
ID	Q8NS57	PRELIMINARY	PRT	339 AA		
AC	Q8NS57					
DT	01-OCT-2002	(TREMBLrel. 22, Created)				
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)				
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)				
OS	GPR17 protein					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo					
OX	NCBI_Taxid=9606					
RY						
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Brain					
RX	MEDLINE=22388257; PubMed=12477932					
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,					
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaeetz T.E.,					
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carinici P., Prange C.,					
RA	Raha S.S., Loguella N.A., Peters G.J., Abrahamson R.D., Mullaly S.J.,					
RA	Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,					

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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X.Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Struhsberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031653; AAH31653.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-..; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PRINTS; PR01157; P2YURNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
SQ SEQUENCE 339 AA; 37860 MW; BB0CAFD0FC371D63 CRC64;

Query Match 26.9%; Score 481.5; DB 2; Length 339;
Best Local Similarity 34.6%; Pred. No. 1.9e-22;
Matches 115; Conservative 62; Mismatches 130; Indels 25; Gaps 10;

QY 16 EMEPNQ--TFSSNNRNCTEN-FKKEFPITYLLIFFMCGVLGNGLSYFLQPYKST 71
DB 5 EVAPPPGLITNPSLTAECQGETLEMLLPASFLITFLITVALVNTALMFFIDHKSQT 64
QY 72 SVNPFMLNALSDLLFTSTLPPRADYLRGSNMIFGLDACRIMSGLSYVMNYSITPLTV 131
DB 65 PANNFMLHVAADLSCVLTPLTRLYHPSGNMFPFGIACLTGFLTYLNNYASITPLTC 124
QY 132 LSVRFPLAMVHPFRLHVTYSIRSAMILGCIWILI-MASSIMLDSGSBQNGSVTSCTEL 190
DB 125 ISADRFPLAIVHPVSKLRPLRYLAHLACAFILMVAVAMAPLIVSPQTVQNHHTVCIQ- 183
QY 191 NLKYIAKLQTMNVTALVGVCLLPFTSTICLLIIRVLAKVEVSGRISRHR--KALT 247
DB 184 -LYR-EKASHNALVSLVAFTFPITVTYCYLILIRSL-----RQGIAREKRLKTRAVR 235
QY 248 TIITTLIIFFCLFPPYHTLRTVHLTWKV-GLCKDLHKALV-ITLATAAANACENPL 303
DB 236 MIALVLAIFLVCPFYPHVNSVYVLAHTRSHASCATQRIALANRITSCITSLNGALDPI 295
QY 304 LYPFAGENFKDLKASL---RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALCNLLCGKRLKGPSPSPBCK 327

Search completed: December 13, 2004, 17:52:34
Job time : 191 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:44:09 ; Search time 40 Seconds
(without alignments)
573.651 Million cell updates/sec

Title: US-09-980-049-1

Perfect score: 1788
Sequence: 1 MERKMSLOPSSISVSEMEPN.....KATKCVFVSWLRKRETV 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/6C.COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1779	99.5	346	4 US-09-585-876-2	Sequence 2, App11
2	559	31.3	337	3 US-09-044-404A-2	Sequence 2, App11
3	559	31.3	337	4 US-09-586-924-2	Sequence 2, App11
4	483.5	27.0	339	1 US-08-153-848-44	Sequence 4, App11
5	483.5	27.0	339	2 US-08-812-871-3	Sequence 3, App11
6	483.5	27.0	339	3 US-09-299-843A-44	Sequence 4, App11
7	483.5	27.0	339	4 US-09-088-337B-44	Sequence 4, App11
8	483.5	27.0	339	5 US-09-170-496D-32	Sequence 3, App11
9	483.5	27.0	339	5 PCT-US93-11153-44	Sequence 4, App11
10	483.5	27.0	339	5 PCT-US95-07180-2	Sequence 2, App11
11	480.5	26.9	339	4 US-09-170-496D-182	Sequence 182, App11
12	464	25.0	362	3 US-08-513-974B-374	Sequence 3, App11
13	447.5	25.0	370	3 US-08-781-250-2	Sequence 2, App11
14	446	24.9	373	4 US-09-745-842-14	Sequence 14, App11
15	442	24.7	373	2 US-08-559-524A-4	Sequence 4, App11
16	442	24.7	373	3 US-08-749-707-4	Sequence 4, App11
17	442	24.7	373	4 US-09-947-922-4	Sequence 4, App11
18	440	24.6	361	1 US-08-383-750-4	Sequence 4, App11
19	440	24.6	361	3 US-08-352-678-4	Sequence 4, App11
20	440	24.6	361	4 US-09-536-954-4	Sequence 4, App11
21	440	24.6	361	4 US-09-170-496D-78	Sequence 78, App11
22	440	24.6	361	4 US-09-929-583B-4	Sequence 4, App11
23	440	24.6	361	5 PCT-US93-0936-4	Sequence 4, App11
24	439.5	24.6	348	3 US-08-852-824-17	Sequence 17, App11
25	439	24.6	302	2 US-08-467-948A-30	Sequence 30, App11
26	439	24.6	302	3 US-08-467-947A-30	Sequence 30, App11
27	437	24.4	344	2 US-08-467-948A-8	Sequence 8, App11

ALIGNMENTS

28	437	24.4	344	3 US-08-467-947A-8	Sequence 8, App11
29	434	24.3	361	4 US-09-170-496D-206	Sequence 206, App11
30	434	24.3	377	4 US-09-745-842-17	Sequence 17, App11
31	424.5	23.7	374	4 US-09-745-842-15	Sequence 15, App11
32	419.5	23.5	373	3 US-08-513-974B-373	Sequence 373, App11
33	419.5	23.5	374	4 US-09-102-710B-3	Sequence 9, App11
34	416	23.3	342	3 US-08-988-876-9	Sequence 2, App11
35	416	23.3	375	1 US-08-442-134A-2	Sequence 2, App11
36	416	23.3	375	1 US-08-444-581B-2	Sequence 2, App11
37	416	23.3	375	1 US-08-446-088A-2	Sequence 3, App11
38	416	23.3	375	2 US-08-559-524A-3	Sequence 3, App11
39	416	23.3	375	3 US-08-749-707-3	Sequence 3, App11
40	416	23.3	375	4 US-09-947-922-3	Sequence 2, App11
41	409.5	22.9	342	4 US-09-054-272-2	Sequence 2, App11
42	406.5	22.7	398	1 US-08-097-938-6	Sequence 6, App11
43	406.5	22.7	398	1 US-08-476-000-6	Sequence 6, App11
44	406.5	22.7	398	1 US-08-472-840-6	Sequence 6, App11
45	406.5	22.7	398	2 US-08-476-976-6	Sequence 6, App11

RESULT 1

US-09-585-876-2
Sequence 2, Application US/09585876
Patent No. 6586205
GENERAL INFORMATION:
APPLICANT: Gluckmann, Maria Alexandra
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
FILE REFERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585, 876
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/182, 061
EARLIER FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-585-876-2

Query Match 99.5%; Score 1779; DB 4; Length 346;
Best Local Similarity 99.4%; Pred. No. 3.7e-131;
Matches 344; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MERKMSLOPSSISVSEMEPNCTTBNFKREFFPIVYLIIFFWGLGNGLSI	60
DB	1	MERKMSLOPSSISVSEMEPNCTTBNFKREFFPIVYLIIFFWGLGNGLSI	60
QY	61	YVFLQYKSTSTNVNMLALSDLFISTLPRAVYIRGSNWIRGDLACRIMSISLVY	120
DB	61	YVFLQYKSTSTNVNMLALSDLFISTLPRAVYIRGSNWIRGDLACRIMSISLVY	120
QY	121	NMTSYIFLVLSVVFPLAMVHPFRLHYTSIRSAWILGIIWILIMASSIMLDGSGQ	180
DB	121	NMTSYIFLVLSVVFPLAMVHPFRLHYTSIRSAWILGIIWILIMASSIMLDGSGQ	180
QY	181	NGSVTSCLEINLYKINKQTMNYIALVVGCLPFFLTSLCYLLIIVLAKVEPBESGLRV	240
DB	181	NGSVTSCLEINLYKINKQTMNYIALVVGCLPFFLTSLCYLLIIVLAKVEPBESGLRV	240
QY	241	SHRKATTTTITLIFFLCFLPYHTLRTVHLTWKVGCLCDRLAKLVITLVAANACP	300
DB	241	SHRKATTTTITLIFFLCFLPYHTLRTVHLTWKVGCLCDRLAKLVITLVAANACP	300
QY	301	NPLLYVFAGENFDRLSALRKQHPQAKTKCVFVSWLRKRETV	346
DB	301	NPLLYVFAGENFDRLSALRKQHPQAKTKCVFVSWLRKRETV	346

RESULT 2

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US-09-044-404A-2
; Sequence 2, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH-70001-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-044-404A-2

```

Query Match 31.3%; Score 559; DB 3; Length 337;

Best Local Similarity 38.0%; Pred. No. 3.6e-36; Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

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27 NSRNC--TIENFKREFFPIVYLIIFWGLANGLSIYFLOPKKSTSVNFMNLAIISD 84
10 SATGCHDITDDPRNQVSTLYSMISVGFPGNGFVLYLIKTHKSAFOVVMINLAIVAD 69
85 LIFISTLPPRADYILRGSNMIFGDLACRIMSYSLVNMYSIYFLTVLSVDFLAMVHP 144
70 LFCVCTLPRLVVVYVHKGIWLFQDFLCRLSTYALVNLCSIFPMTAMSPFCIAIVFPV 129
145 RLIAHTSIRSAWILGIIWI-LIMASSIMLDSGSEONGSVTSCLEMLYKIAK--LQTM 201
130 QNINLVTKKARFVCGVIMIPVILTSPPFLMAKPKQDKGNNTKCFEPPODNOTKNHVLV 189
202 NYIALVVGCLPFFLTSLICYLIIIRVLKVEVPSGLRVSHRKALTTIITLIIFFLCFL 261
190 HYVSLFVGFIIIPVLIIVCYTMIITLLKSKMKN--LSHKKAKGIMIVVTAAPLVFSM 247
262 PYHTLRTVHLTTW--KVGLCSD--RLHKAIVTTLAALANACNPLLYYPAGEPFDRILK 317

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Db 248 PYHIOHTIHLPHNETKPCDSVLRMOKSVITLTLAASNCCEPDLVYFGSGNFRKRL- 306
QY 318 SALRK 322
Db 307 STFRK 311

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RESULT 3

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US-09-586-924-2
; Sequence 2, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH M.
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELLIS, CATHERINE E.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: CHAMBERS, JON
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL
; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
; FILE REFERENCE: GH-70001-ID1
; CURRENT APPLICATION NUMBER: US/09/586,924
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 09/044,404
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/844,795
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-586-924-2

```

Query Match 31.3%; Score 559; DB 4; Length 337;

Best Local Similarity 38.0%; Pred. No. 3.6e-36; Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

```

27 NSRNC--TIENFKREFFPIVYLIIFWGLANGLSIYFLOPKKSTSVNFMNLAIISD 84
10 SATGCHDITDDPRNQVSTLYSMISVGFPGNGFVLYLIKTHKSAFOVVMINLAIVAD 69
85 LIFISTLPPRADYILRGSNMIFGDLACRIMSYSLVNMYSIYFLTVLSVDFLAMVHP 144
70 LFCVCTLPRLVVVYVHKGIWLFQDFLCRLSTYALVNLCSIFPMTAMSPFCIAIVFPV 129
145 RLIAHTSIRSAWILGIIWI-LIMASSIMLDSGSEONGSVTSCLEMLYKIAK--LQTM 201
130 QNINLVTKKARFVCGVIMIPVILTSPPFLMAKPKQDKGNNTKCFEPPODNOTKNHVLV 189
202 NYIALVVGCLPFFLTSLICYLIIIRVLKVEVPSGLRVSHRKALTTIITLIIFFLCFL 261
190 HYVSLFVGFIIIPVLIIVCYTMIITLLKSKMKN--LSHKKAKGIMIVVTAAPLVFSM 247
262 PYHTLRTVHLTTW--KVGLCSD--RLHKAIVTTLAALANACNPLLYYPAGEPFDRILK 317
248 PYHIOHTIHLPHNETKPCDSVLRMOKSVITLTLAASNCCEPDLVYFGSGNFRKRL- 306
QY 318 SALRK 322
Db 307 STFRK 311

```

RESULT 4

```

US-08-153-848-44
; Sequence 44, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.

```

TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-44

Query Match 27.0%; Score 483.5; DB 1; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

QY 16 EMBPNC--TFSSNNNSNCTIEN-FKREPPYVLIIFPMGVGNGSIYFLOPYKST 71
DB 5 EVAPPGIITFSLATBQCGQETPLENMLPASFYLDLFIALVGNLTALMLFIRDKSGT 64
QY 72 SVNVFMLNTAISDLFIISTLPFRADYYLRGSNMIFGDLACRIMSLSLYNMYSIYFLTV 131
DB 65 PAVVFLMHLAVADLSCLVLPTRLYVHFGSNHMPFGELACRLTGFLYLMVYSIYFLTC 124
QY 132 LSVVRFLAMVHPRLHVTISIRSAMILCGIITWLI-MASSIMLLDGSSENGSVTSCLEL 190
DB 125 ISADRFALIVHPVKSILRRPLVYHMLACAFLMVVAVAMAPLVSPQTVQTNHTVCLQ- 183
QY 191 NLKIKALQTMNTIALVVGCLPFTISICYLLIIRVLKVEVBSGLRVSHR---KALT 247
DB 184 -LVR-EKASHRALVSLAVAFPTPTTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
QY 248 TIIITLIIIFLCPLPYHTLRTVHLTTWKV--GLCKDLHKALV--ITLALAAANACFNPL 303
DB 236 MIALVLAIFVLCVPYVHRSVYVLAHRSHGASCATORIALANRITSCLSLNGALDPI 295
QY 304 LYYFAGENPKDRLSAL---RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALCNLLCGKRLKQPPSPFGK 327

RESULT 5
US-08-812-871-3
Sequence 3, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice

APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
City: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 992700
US-08-812-871-3

Query Match 27.0%; Score 483.5; DB 2; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

QY 16 EMBPNC--TFSSNNNSNCTIEN-FKREPPYVLIIFPMGVGNGSIYFLOPYKST 71
DB 5 EVAPPGIITFSLATBQCGQETPLENMLPASFYLDLFIALVGNLTALMLFIRDKSGT 64
QY 72 SVNVFMLNTAISDLFIISTLPFRADYYLRGSNMIFGDLACRIMSLSLYNMYSIYFLTV 131
DB 65 PAVVFLMHLAVADLSCLVLPTRLYVHFGSNHMPFGELACRLTGFLYLMVYSIYFLTC 124
QY 132 LSVVRFLAMVHPRLHVTISIRSAMILCGIITWLI-MASSIMLLDGSSENGSVTSCLEL 190
DB 125 ISADRFALIVHPVKSILRRPLVYHMLACAFLMVVAVAMAPLVSPQTVQTNHTVCLQ- 183
QY 191 NLKIKALQTMNTIALVVGCLPFTISICYLLIIRVLKVEVBSGLRVSHR---KALT 247
DB 184 -LVR-EKASHRALVSLAVAFPTPTTVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
QY 248 TIIITLIIIFLCPLPYHTLRTVHLTTWKV--GLCKDLHKALV--ITLALAAANACFNPL 303
DB 236 MIALVLAIFVLCVPYVHRSVYVLAHRSHGASCATORIALANRITSCLSLNGALDPI 295
QY 304 LYYFAGENPKDRLSAL---RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALCNLLCGKRLKQPPSPFGK 327

RESULT 6
US-09-299-843A-44

```
/ Sequence 44, Application US/09299843A
/ Patent No. 6107475
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schwellkart, Vicki L.
/ TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/299,843A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 09/088,337
/ FILING DATE: 01-JUN-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/153,848
/ FILING DATE: 17-NOV-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jill E. Uhl
/ REGISTRATION NUMBER: 43,213
/ REFERENCE/DOCKET NUMBER: 27866/32059B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-299-843A-44

Query Match      27.0%; Score 483.5; DB 3; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;
```

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QY      304 LYYFAGENPKORLKSAL-----RKGHPOKAKTK 331
DB      296 MYFVAEKPRHALCNLGGKRLKGPSPFEGK 327

RESULT 7
US-09-088-337B-44
/ Sequence 44, Application US/09088337B
/ Patent No. 6348574
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schwellkart, Vicki L.
/ TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/088,337B
/ FILING DATE: 01-Jun-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/153,848
/ FILING DATE: 17-NOV-1993
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6348574and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

Query Match      27.0%; Score 483.5; DB 3; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;
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Db 184 -LYR-EKASHALVSLAVALFTPTTTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
 QY 248 TITITLIFPLCPPLPYHTLTTHLTKV--GLCKDLHKAIV--ITLALAAANACPNPL 303
 Db 236 MIAIVLAIFVCFVPHVNSVYVLAHRSHGASCATRIALANRITSCLTSLNGALDPI 295
 QY 304 LYFAGENFDRLKSLA---RKGHPOKATK 331
 Db 296 MYFFVAEKFRHALCNLLCGKRLKGPSPFSGK 327

RESULT 8

US-09-170-496D-32
 ; Sequence 32, Application US/09170496D
 ; Patent No. 6555339
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
 ; TITLE OF INVENTION: Receptors
 ; FILE REFERENCE: AEN-0040
 ; CURRENT APPLICATION NUMBER: US/09/170,496D
 ; CURRENT FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 294
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 32
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-170-496D-32

Query Match 27.0%; Score 483.5; DB 4; Length 339;
 Best Local Similarity 34.6%; Pred. No. 2,7e-30;
 Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;
 QY 16 EMBPG---TFSNNNSRNCITEN-FKREFPPIVYLIIFFMGVGLNGLSIVFLQPYKST 71
 Db 5 EVAPPGIITNFSLATACQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDKSGT 64
 QY 72 SVNVFMLNLASDLFIISTLPFRADYYLRGSMNIFGDLACRIMSYSLYVMYSIYFLTV 131
 Db 65 PAVVFLHIALVADISCVLPTRLYVHFSGNHMPFSGIACRLTGLFLYLMYASIFLTC 124
 QY 132 LSVVRFAMVHPRFLHTVTSIRSAWILGIIWILI-MASSIMLDGSGEONGSVTSCLT 190
 Db 125 ISADRFLAVHPYKSLKRLRPVLAHLACAFLMVVAWAPLIVSPQTVQTNHTVCLQ- 183
 QY 191 NLTKIAQLQTMNTIALVVGCLLPFTLSICYLIIIVLKVVEVBSGLRVSHR---KALT 247
 Db 184 -LYR-EKASHALVSLAVALFTPTTTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
 QY 248 TITITLIFPLCPPLPYHTLTTHLTKV--GLCKDLHKAIV--ITLALAAANACPNPL 303
 Db 236 MIAIVLAIFVCFVPHVNSVYVLAHRSHGASCATRIALANRITSCLTSLNGALDPI 295
 QY 304 LYFAGENFDRLKSLA---RKGHPOKATK 331
 Db 296 MYFFVAEKFRHALCNLLCGKRLKGPSPFSGK 327

RESULT 9
 PCT-US93-11153-44
 ; Sequence 44, Application PC/TUS9311153
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schenkart, Vicki L.
 ; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESS: Bicknell

STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11153
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Noland, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELETYPE: 25-3856
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US93-11153-44

Query Match 27.0%; Score 483.5; DB 5; Length 339;
 Best Local Similarity 34.6%; Pred. No. 2,7e-30;
 Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;
 QY 16 EMBPG---TFSNNNSRNCITEN-FKREFPPIVYLIIFFMGVGLNGLSIVFLQPYKST 71
 Db 5 EVAPPGIITNFSLATACQCGQETPLENMLFASFYLLDFILALVGNLTALMLFIRDKSGT 64
 QY 72 SVNVFMLNLASDLFIISTLPFRADYYLRGSMNIFGDLACRIMSYSLYVMYSIYFLTV 131
 Db 65 PAVVFLHIALVADISCVLPTRLYVHFSGNHMPFSGIACRLTGLFLYLMYASIFLTC 124
 QY 132 LSVVRFAMVHPRFLHTVTSIRSAWILGIIWILI-MASSIMLDGSGEONGSVTSCLT 190
 Db 125 ISADRFLAVHPYKSLKRLRPVLAHLACAFLMVVAWAPLIVSPQTVQTNHTVCLQ- 183
 QY 191 NLTKIAQLQTMNTIALVVGCLLPFTLSICYLIIIVLKVVEVBSGLRVSHR---KALT 247
 Db 184 -LYR-EKASHALVSLAVALFTPTTTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
 QY 248 TITITLIFPLCPPLPYHTLTTHLTKV--GLCKDLHKAIV--ITLALAAANACPNPL 303
 Db 236 MIAIVLAIFVCFVPHVNSVYVLAHRSHGASCATRIALANRITSCLTSLNGALDPI 295
 QY 304 LYFAGENFDRLKSLA---RKGHPOKATK 331
 Db 296 MYFFVAEKFRHALCNLLCGKRLKGPSPFSGK 327

RESULT 10
 PCT-US95-07180-2
 ; Sequence 2, Application PC/TUS9507180
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, YI
 ; APPLICANT: GOCAYNE, JEANINE D
 ; APPLICANT: RUBEN, STEVEN M
 ; TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,


```

RESULT 11
US-09-170-496D-182
; Sequence 182, Application US/09170496D
; Patent No. 655539
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655539-Endogenous, Constitutively Activated Human G Protein
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AEPN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294

```

RESULT 12
 US-08-513-974B-374
 Sequence 374, Application US/08513974B
 Patent No. 6114139
 GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Maasaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Onitaki, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Ohgi, Kazuhiko
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BROWNSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 City: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093969
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:

Query Match	26.0%	Score 464	DB 3	Length 362	
Best Local Similarity	30.6%	Pred. No. 9.5e-29			
Matches	99	Conservative	82	Mismatches 117	Indels 26
				Gaps	7
Qy	16	EMEBNGTFSSNNNSRNCIT-ENFKRKEFPPIYLLIFFWGLNGSLSYVFLDPQYKKSISV	73		
Db	16	ELLAGGMAAGNATTKCSLTKTGFGYYVLPPTYVILVIFGIGLNSVALIMWPFPHMRPMGCI	75		
Qy	74	NVFMNLALISDLPISTIPPRADYYLIRBSNNMIFGLARINSYSLYNMYSIYLTYS	133		
Db	76	SVVMFNALAPFLVYLTLPALIPFYFNKTDWIFGVMCKLRFPIHVALYSGISLFLTGIS	135		
Qy	134	VVREIAMVHPRLIHTVTSIRSAWILCGIITLIMASSIMLT---DSGEONGSVTSCL	189		
Db	136	VHRTGVVHPKSLGRLKKGAAYVSSLYMVALVAVIPIFYSIGVRKKIT-CYDT	194		
Qy	190	-----LNIYKIAKLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPSGLRVSHRK	244		
Db	195	TADELRSYFPYVSMCTVFMFCI-----PFIYILGCGYLIYKALYIKOLDNSPLR---RK	246		
Qy	245	ALTTIIILILIFPLCFELPYHTLRVHL-----TWKRGKGLCKDRILKALVITLMAANA	298		
Db	247	STYVILYILVTPAVSYLPEFHWKTLINLPAARDLPOTPMQCAFNDKVATATYQVTRGLASINS	306		
Qy	299	CENPLLYYFAGENFQDRLKSLARK	322		
Db	307	CVDPIYVLAGDTFRRRLSRATRK	330		

[illegible]

RESULT 14
US-09-745-842-14
Sequence 14, Application US/09745842
Patent No. 6762029
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
APPLICANT: Ramakrishnan-Dubridge, Vanitha
APPLICANT: Julius, David
APPLICANT: Holloper, Gunter
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: P2Y12 Receptor
FILE REFERENCE: 44481-5053-US
CURRENT APPLICATION NUMBER: US/09/745,842
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 60/171,622
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 373
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
US-09-745-842-14

Query Match 24.9%; Score 446; DB 4; Length 373;
Best Local Similarity 32.1%; Pred. No. 2.5e-27;
Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

QY 22 TSNNSRNC--TIENFKREFFPIVYLIIFFWGVNGLSIYVFLQPKKSTSVNFMNL 79
DB 33 TAAVSSFCALTKTGFORYYLPAYTILVFIIGFLGNSVAIMWFPHMKPMSSISYVFN 92
QY 80 LAISDLFIISTLPFRADYILRGSMWIFGDLACRIMSYSLVNMYSIYFVLVSVRFLA 139
DB 93 LMLADFLVYLTPALIFYFNKTDWIFGDMCKLQRFPHVNLGSLFLTCSAHRYSYG 152
QY 140 MHHPFLVHTSIRSMWILGIIW-ILMASSIMLDGSG--EONGSVTSCLE-----L 190
DB 153 VVYPLSLRLKKNKICISVLMVLVVAISPILFYSIGVAKNKTIIT-CYDTTSDEYL 211
QY 191 NYKIAKLOTMYIALVWGCLPEFTLSICYLLIRVLKVEVPSGLRVSHRKALTTII 250
DB 212 RSYFISMTCT---TVAMFC-VPLVILIGCYGLIVALIVKDDNSPLR--RKSIVLYI 263
QY 251 ITLLIFPLCLPYHTLRTVHLTT---WKVGLC--KDLHLKALVITLALAAANACFNPPL 304
DB 264 IYLVFAVASYIPHWKTMNLRARLDFOTPMCAFNDRVATYQVTRGLASLNSCVDPI 323
QY 305 YYPAGENFKDLKSLARK 322
DB 324 YFLAGDTFRRRLSRATRK 341

RESULT 15
US-08-559-524A-4
Sequence 4, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-4

Query Match 24.7%; Score 442; DB 2; Length 373;
Best Local Similarity 31.0%; Pred. No. 5.1e-27;
Matches 95; Conservative 78; Mismatches 109; Indels 24; Gaps 7;

QY 32 TIENFKREFFPIVYLIIFFWGVNGLSIYVFLQPKKSTSVNFMNLAIISDLFIISTL 91
DB 45 TKTGFQFYLLPAVYILVFIIGFLGNSVAIMWFPHMKPMSSISYVFNMLADFLVYL 104
QY 92 PFRADYILRGSMWIFGDLACRIMSYSLVNMYSIYFVLVSVRFLAMHPRLLHTS 151
DB 105 PALIFYFNKTDWIFGDMCKLQRFPHVNLGSLFLTCSAHRYSGVVYPLKSLGRK 164
QY 152 ISAWILGIIWILMASSIML---DSGSEONGSVTSCLE-----INLYKIAKLOTWN 202
DB 165 KNAVAYISVVLIVVAGISPLFYSIGVIRKNKTIIT-CYDTTSDEYLRSYIYSMTCT-- 221
QY 203 YIALVWGCLPEFTLSICYLLIRVLKVEVPSGLRVSHRKALTTIIITLLIFPLCLP 262
DB 222 --TVAMFC-VPLVILIGCYGLIVALIVKDDNSPLR--RKSIVLYIIVLVFAVSYP 275
QY 263 YHTLRTVHL-----TTMKVGLCKRDLKALVITLALAAANACFNPPLYYPGENFKRL 316
DB 276 FHWKTMNLRARLDFOTPMCAFNDRVATYQVTRGLASLNSCVDPIYFLAGDTFRRRL 335
QY 317 KSLARK 322
DB 336 SRATRK 341

Search completed: December 13, 2004, 17:54:06
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:52:40 ; Search time 148 Seconds

(Without alignments)
835.025 Million cell updates/sec

Title: US-09-980-049-1

Perfect score: 1788
Sequence: 1 MERKFSLOPISVSSEMEPN.....KATKCVFVSWLRKRETV 346Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1788	100.0	346	US-09-826-791-6	Sequence 6, Appl1
2	1788	100.0	346	US-09-866-230-7	Sequence 7, Appl1
3	1788	100.0	346	US-09-866-230-9	Sequence 9, Appl1
4	1788	100.0	346	US-09-828-478-2	Sequence 2, Appl1
5	1788	100.0	346	US-09-779-679-2	Sequence 2, Appl1
6	1788	100.0	346	US-09-779-679-26	Sequence 26, Appl1
7	1788	100.0	346	US-09-891-225-30	Sequence 30, Appl1
8	1788	100.0	346	US-09-980-049-1	Sequence 1, Appl1
9	1788	100.0	346	US-10-225-567A-589	Sequence 589, Appl1
10	1788	100.0	346	US-10-349-021-2	Sequence 2, Appl1
11	1788	100.0	346	US-10-321-807-14	Sequence 14, Appl1
12	1788	100.0	346	US-10-131-332A-2	Sequence 2, Appl1
13	1788	100.0	346	US-10-369-405-30	Sequence 30, Appl1

14	1788	100.0	346	US-10-182-605-2	Sequence 2, Appl1
15	1788	100.0	346	US-10-403-161-22	Sequence 22, Appl1
16	1788	100.0	346	US-10-403-161-24	Sequence 24, Appl1
17	1788	100.0	346	US-10-343-650A-58	Sequence 58, Appl1
18	1788	100.0	346	US-10-297-247-2	Sequence 2, Appl1
19	1788	100.0	346	US-10-321-807-14	Sequence 14, Appl1
20	1788	100.0	346	US-10-314-048A-14	Sequence 14, Appl1
21	1788	100.0	346	US-10-757-262-40	Sequence 40, Appl1
22	1782	99.7	346	US-10-321-807-88	Sequence 88, Appl1
23	1782	99.7	346	US-10-321-807-88	Sequence 88, Appl1
24	1782	99.7	346	US-10-314-048A-88	Sequence 88, Appl1
25	1762	98.5	341	US-09-991-225-55	Sequence 55, Appl1
26	1762	98.5	341	US-10-369-405-55	Sequence 55, Appl1
27	1712	95.7	330	US-09-826-791-2	Sequence 2, Appl1
28	1712	95.7	330	US-09-991-225-2	Sequence 2, Appl1
29	1712	95.7	330	US-10-369-405-2	Sequence 2, Appl1
30	1712	95.7	330	US-10-775-965-110	Sequence 110, Appl1
31	612	34.2	126	US-10-296-115-1356	Sequence 1356, Appl1
32	564	31.5	337	US-10-290-078-21	Sequence 21, Appl1
33	559	31.3	337	US-09-866-230-8	Sequence 8, Appl1
34	559	31.3	337	US-09-828-478-5	Sequence 5, Appl1
35	559	31.3	337	US-09-779-679-27	Sequence 27, Appl1
36	559	31.3	337	US-09-991-225-6	Sequence 6, Appl1
37	559	31.3	337	US-10-055-106C-3	Sequence 3, Appl1
38	559	31.3	337	US-10-225-567A-547	Sequence 547, Appl1
39	559	31.3	337	US-10-349-021-5	Sequence 5, Appl1
40	559	31.3	337	US-10-369-405-6	Sequence 6, Appl1
41	559	31.3	337	US-10-692-605-4	Sequence 4, Appl1
42	557	31.2	337	US-10-167-192-3	Sequence 3, Appl1
43	557	31.2	337	US-10-400-991-6	Sequence 6, Appl1
44	487.5	27.3	337	US-09-943-198-4	Sequence 4, Appl1
45	487.5	27.3	337	US-09-885-453-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-826-791-6
Sequence 6, Application US/09826791
Patent No. US20010039037A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
FILE OF INVENTION: NO. US20010039037A1et Polypeptide
TITLE REFERENCE: PCT0914ADAM
CURRENT APPLICATION NUMBER: US/09/826,791
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/198,367
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-791-6

Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFSLOPISVSSEMEPNCTENKREFFPIVLIIFPMGVLAGNGLST 60
DB 1 MERKFSLOPISVSSEMEPNCTENKREFFPIVLIIFPMGVLAGNGLST 60
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DB 61 YVFLQYKSTSVNFMALASDLFIPTLPFRADYLRGSNWTGDLACRIMSYSLV 120
QY 121 NMVSSYPLTVLSVRFLLMVFHFRLLHTSIRSAWILGIIWILMASSIMLDGSGSEQ 180
DB 121 NMVSSYPLTVLSVRFLLMVFHFRLLHTSIRSAWILGIIWILMASSIMLDGSGSEQ 180

Db 121 NMYSSIFLTVLSVRFAMVHFRLLHVTIRSAMWLGIIIMLMASSIMLDSGSEQ 180
QY 181 NSGVSCLBLNLYKIAKQTMNIALVVGCLLPFFLTSLCYLLIIVLAKVEPESGLRV 240
Db 181 NSGVSCLBLNLYKIAKQTMNIALVVGCLLPFFLTSLCYLLIIVLAKVEPESGLRV 240
QY 241 SHRKALTTIIITLIIIFLCELPYHTLRVHTLTMWKVGLCKDRLHKLAVITLALAAACF 300
Db 241 SHRKALTTIIITLIIIFLCELPYHTLRVHTLTMWKVGLCKDRLHKLAVITLALAAACF 300
QY 301 NPLLYYPAGEENFKDRLKSLARKGHPQAKTKCVFPVSWLKRKTRV 346
Db 301 NPLLYYPAGEENFKDRLKSLARKGHPQAKTKCVFPVSWLKRKTRV 346

RESULT 2
US-09-866-230-7
; Sequence 7, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.
; TITLE OF INVENTION: No. US20020150901A1e1 Nucleic Acids, Polypeptides, Methods of Mak
; FILE REFERENCE: REG 771A
; CURRENT APPLICATION NUMBER: US/09/866,230
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,725
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 346
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-866-230-7

Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEBNGTFSSNNRNCTIENFKKEFPPIVYLIIFPMGVLAGNGLSI 60
Db 1 MERKFMSLQPSISVSSEMEBNGTFSSNNRNCTIENFKKEFPPIVYLIIFPMGVLAGNGLSI 60
QY 61 YVFLQPKKSTSVNVFMNLAIISDLLEFISTLPFRADYYLRGSNWIFGDLACRIMSYSLVY 120
Db 61 YVFLQPKKSTSVNVFMNLAIISDLLEFISTLPFRADYYLRGSNWIFGDLACRIMSYSLVY 120
QY 121 NMYSSIFLTVLSVRFAMVHFRLLHVTIRSAMWLGIIIMLMASSIMLDSGSEQ 180
Db 121 NMYSSIFLTVLSVRFAMVHFRLLHVTIRSAMWLGIIIMLMASSIMLDSGSEQ 180
QY 181 NSGVSCLBLNLYKIAKQTMNIALVVGCLLPFFLTSLCYLLIIVLAKVEPESGLRV 240
Db 181 NSGVSCLBLNLYKIAKQTMNIALVVGCLLPFFLTSLCYLLIIVLAKVEPESGLRV 240
QY 241 SHRKALTTIIITLIIIFLCELPYHTLRVHTLTMWKVGLCKDRLHKLAVITLALAAACF 300
Db 241 SHRKALTTIIITLIIIFLCELPYHTLRVHTLTMWKVGLCKDRLHKLAVITLALAAACF 300
QY 301 NPLLYYPAGEENFKDRLKSLARKGHPQAKTKCVFPVSWLKRKTRV 346
Db 301 NPLLYYPAGEENFKDRLKSLARKGHPQAKTKCVFPVSWLKRKTRV 346

RESULT 3
US-09-866-230-9
; Sequence 9, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.
; TITLE OF INVENTION: No. US20020150901A1e1 Nucleic Acids, Polypeptides, Methods of Mak
; FILE REFERENCE: REG 771A
; CURRENT APPLICATION NUMBER: US/09/866,230

; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,725
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 346
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-866-230-9

Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEBNGTFSSNNRNCTIENFKKEFPPIVYLIIFPMGVLAGNGLSI 60
Db 1 MERKFMSLQPSISVSSEMEBNGTFSSNNRNCTIENFKKEFPPIVYLIIFPMGVLAGNGLSI 60
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Db 61 YVFLQPKKSTSVNVFMNLAIISDLLEFISTLPFRADYYLRGSNWIFGDLACRIMSYSLVY 120
QY 121 NMYSSIFLTVLSVRFAMVHFRLLHVTIRSAMWLGIIIMLMASSIMLDSGSEQ 180
Db 121 NMYSSIFLTVLSVRFAMVHFRLLHVTIRSAMWLGIIIMLMASSIMLDSGSEQ 180
QY 181 NSGVSCLBLNLYKIAKQTMNIALVVGCLLPFFLTSLCYLLIIVLAKVEPESGLRV 240
Db 181 NSGVSCLBLNLYKIAKQTMNIALVVGCLLPFFLTSLCYLLIIVLAKVEPESGLRV 240
QY 241 SHRKALTTIIITLIIIFLCELPYHTLRVHTLTMWKVGLCKDRLHKLAVITLALAAACF 300
Db 241 SHRKALTTIIITLIIIFLCELPYHTLRVHTLTMWKVGLCKDRLHKLAVITLALAAACF 300
QY 301 NPLLYYPAGEENFKDRLKSLARKGHPQAKTKCVFPVSWLKRKTRV 346
Db 301 NPLLYYPAGEENFKDRLKSLARKGHPQAKTKCVFPVSWLKRKTRV 346

RESULT 4
US-09-828-478-2
; Sequence 2, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-828-478-2

Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MERKFMSLQPSISVSSEMEBNGTFSSNNRNCTIENFKKEFPPIVYLIIFPMGVLAGNGLSI 60
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Db 61 YVFLQPYKSTSVNFMNLAIISDLFIISTLPFRADYYLRGSMWIFGDLACRIMSYSLV 120
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Db 121 NMYSIYFLTVLSVVRFLAVHPRLHVTISRSAMILGIIWILMASSIMLDGSEQ 180
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Db 181 NGVTSCLBLNKYKIAKIQTMNYIALVGCILPFTLSICYLIIIRVLKVEPESGLRV 240
QY 241 SHRKALTTIIITLIIFLFCPLPYHTLRVHLTTWKVGLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLFCPLPYHTLRVHLTTWKVGLCKDRHLKALVITLALAAACF 300
QY 301 NPLIYFAGNFKDRLSALRKHPQAKTKCVFVSWLRKETR 346
Db 301 NPLIYFAGNFKDRLSALRKHPQAKTKCVFVSWLRKETR 346

RESULT 5

US-09-779-679-2
Sequence 2, Application US/09779679
Publication No. US20030082757A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchertnev, Velizar T
APPLICANT: Mishra, Vishnu S
APPLICANT: Casman, Stacie
APPLICANT: Ballinger, Robert
APPLICANT: Vermet, Corine A
APPLICANT: Li, Li
APPLICANT: Spytek, Kimberly A
APPLICANT: Andrew, David P
APPLICANT: Mezes, Peter S
TITLE OF INVENTION: No. US20030082757A1 Proteins and Nucleic Acids Encoding the Same
FILE REFERENCE: 15966-661
CURRENT APPLICATION NUMBER: US/09/779, 679
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/181391
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/180, 929
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/219758
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181339
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: USSN 60/181392
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/219585
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181157
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-679-2

Query Match 100.0%; Score 1788; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 MERKFMSLQPSISVSEMEPMTGTFNNNSRNCTIENFKREFFPIYVLIIFPMGVLGNGLSI 60
QY 61 YVFLQPYKSTSVNFMNLAIISDLFIISTLPFRADYYLRGSMWIFGDLACRIMSYSLV 120
Db 61 YVFLQPYKSTSVNFMNLAIISDLFIISTLPFRADYYLRGSMWIFGDLACRIMSYSLV 120
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Db 121 NMYSIYFLTVLSVVRFLAVHPRLHVTISRSAMILGIIWILMASSIMLDGSEQ 180
QY 181 NGVTSCLBLNKYKIAKIQTMNYIALVGCILPFTLSICYLIIIRVLKVEPESGLRV 240
Db 181 NGVTSCLBLNKYKIAKIQTMNYIALVGCILPFTLSICYLIIIRVLKVEPESGLRV 240
QY 241 SHRKALTTIIITLIIFLFCPLPYHTLRVHLTTWKVGLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLFCPLPYHTLRVHLTTWKVGLCKDRHLKALVITLALAAACF 300
QY 301 NPLIYFAGNFKDRLSALRKHPQAKTKCVFVSWLRKETR 346
Db 301 NPLIYFAGNFKDRLSALRKHPQAKTKCVFVSWLRKETR 346

RESULT 6

US-09-779-679-26
Sequence 26, Application US/09779679
Publication No. US20030082757A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchertnev, Velizar T
APPLICANT: Mishra, Vishnu S
APPLICANT: Casman, Stacie
APPLICANT: Ballinger, Robert
APPLICANT: Vermet, Corine A
APPLICANT: Li, Li
APPLICANT: Spytek, Kimberly A
APPLICANT: Andrew, David P
APPLICANT: Mezes, Peter S
TITLE OF INVENTION: No. US20030082757A1 Proteins and Nucleic Acids Encoding the Same
FILE REFERENCE: 15966-661
CURRENT APPLICATION NUMBER: US/09/779, 679
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/181391
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/180, 929
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/219758
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181339
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: USSN 60/181392
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/219585
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181157
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-679-26

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Query Match          100.0%; Score 1788; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREFFPIVYLIIFPWGVLNGLSI 60
DB 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREFFPIVYLIIFPWGVLNGLSI 60
QY 61 YVFLQPKKSTSVNVFMNLAIISDLFIPTLPFRADYLRGSNWIFGDLACRIMSYSLYV 120
DB 61 YVFLQPKKSTSVNVFMNLAIISDLFIPTLPFRADYLRGSNWIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTYSIRSAMIIGIIMWILMASSIMLDSGSEQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTYSIRSAMIIGIIMWILMASSIMLDSGSEQ 180
QY 181 NGSVTSCELEMLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NGSVTSCELEMLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
DB 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
QY 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346
DB 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346

RESULT 7
US-09-991-225-30
; Sequence 30, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBRMY11, EXPRESSED HI
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-225-30

Query Match          100.0%; Score 1788; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREFFPIVYLIIFPWGVLNGLSI 60
DB 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREFFPIVYLIIFPWGVLNGLSI 60
QY 61 YVFLQPKKSTSVNVFMNLAIISDLFIPTLPFRADYLRGSNWIFGDLACRIMSYSLYV 120
DB 61 YVFLQPKKSTSVNVFMNLAIISDLFIPTLPFRADYLRGSNWIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTYSIRSAMIIGIIMWILMASSIMLDSGSEQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTYSIRSAMIIGIIMWILMASSIMLDSGSEQ 180
QY 181 NGSVTSCELEMLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NGSVTSCELEMLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
DB 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
QY 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346
DB 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346
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QY 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
DB 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
QY 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346
DB 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346

RESULT 8
US-09-980-049-1
; Sequence 1, Application US/09980049
; Publication No. US20040220092A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Fairah A.
; APPLICANT: NGUYEN, Danielle B.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LAL, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HAPALIA, April
; APPLICANT: WALIA, Nandinder K.
; APPLICANT: DAS, Debopriya
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0072 PCT
; CURRENT APPLICATION NUMBER: US/09/980,049
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
; PRIOR FILING DATE: 2000-03-29; 2000-04-06; 2000-04-20; 2000-04-28; 2000-05-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 5628963CD1
US-09-980-049-1

Query Match          100.0%; Score 1788; DB 12; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREFFPIVYLIIFPWGVLNGLSI 60
DB 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREFFPIVYLIIFPWGVLNGLSI 60
QY 61 YVFLQPKKSTSVNVFMNLAIISDLFIPTLPFRADYLRGSNWIFGDLACRIMSYSLYV 120
DB 61 YVFLQPKKSTSVNVFMNLAIISDLFIPTLPFRADYLRGSNWIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTYSIRSAMIIGIIMWILMASSIMLDSGSEQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTYSIRSAMIIGIIMWILMASSIMLDSGSEQ 180
QY 181 NGSVTSCELEMLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NGSVTSCELEMLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
DB 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVITLALAAANACF 300
QY 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346
DB 301 NPLLYFAGENFKDRLKSALRKGHPOKATKCVFVSVMLRKETRV 346
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Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 9
US-10-225-567A-589
; Sequence 589, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 589
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-589

Query Match 100.0%; Score 1788; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 36-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMNSLOPSISVSEMEPNGTFSNNNSRNCITENPKRBPPIYVLIIFPMGVANGLSI 60
Db 1 MERKFMNSLOPSISVSEMEPNGTFSNNNSRNCITENPKRBPPIYVLIIFPMGVANGLSI 60

QY 61 YVFLQPKKSTSVNVFNLALISDLPISTLPPRADYYLRGNSWIFGDLACRIMSYSLYV 120
Db 61 YVFLQPKKSTSVNVFNLALISDLPISTLPPRADYYLRGNSWIFGDLACRIMSYSLYV 120

QY 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISASAWILCGIWIILMASSIMLDSGSEQ 180
Db 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISASAWILCGIWIILMASSIMLDSGSEQ 180

QY 181 NGSVTSCLELNLYKIAKQTMNTYIALVVGCLPFTLSICYLIIIRYLKVEVPSGLRV 240
Db 181 NGSVTSCLELNLYKIAKQTMNTYIALVVGCLPFTLSICYLIIIRYLKVEVPSGLRV 240

QY 241 SHRKALTTIIITLIIFLCELPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLCELPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAACF 300

QY 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346
Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 10
US-10-349-021-2
; Sequence 2, Application US/10349021
; Publication No. US20030157541A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/10/349,021
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-349-021-2

Query Match 100.0%; Score 1788; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 36-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMNSLOPSISVSEMEPNGTFSNNNSRNCITENPKRBPPIYVLIIFPMGVANGLSI 60
Db 1 MERKFMNSLOPSISVSEMEPNGTFSNNNSRNCITENPKRBPPIYVLIIFPMGVANGLSI 60

QY 61 YVFLQPKKSTSVNVFNLALISDLPISTLPPRADYYLRGNSWIFGDLACRIMSYSLYV 120
Db 61 YVFLQPKKSTSVNVFNLALISDLPISTLPPRADYYLRGNSWIFGDLACRIMSYSLYV 120

QY 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISASAWILCGIWIILMASSIMLDSGSEQ 180
Db 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISASAWILCGIWIILMASSIMLDSGSEQ 180

QY 181 NGSVTSCLELNLYKIAKQTMNTYIALVVGCLPFTLSICYLIIIRYLKVEVPSGLRV 240
Db 181 NGSVTSCLELNLYKIAKQTMNTYIALVVGCLPFTLSICYLIIIRYLKVEVPSGLRV 240

QY 241 SHRKALTTIIITLIIFLCELPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLCELPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAACF 300

QY 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346
Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 11
US-10-321-807-14
; Sequence 14, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: ARENO086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14

LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-10-321-807-14

Query Match 100.0%; Score 1788; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKMSLOPSTISVSSEMEPNGTFSNNNSRNCCTIENKREFFPIVYLIIFPWGVLGNGLSI 60
DB 1 MERKMSLOPSTISVSSEMEPNGTFSNNNSRNCCTIENKREFFPIVYLIIFPWGVLGNGLSI 60
QY 61 YVFLQPYKKSSTSVNVMNLAIISDLFLSTLPFRADYLRGSNWIIFGDLACRIMSYSLYV 120
DB 61 YVFLQPYKKSSTSVNVMNLAIISDLFLSTLPFRADYLRGSNWIIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTISRANILCGIILWILIMASSIMLDGSGSQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTISRANILCGIILWILIMASSIMLDGSGSQ 180
QY 181 NSGVSCELEINLYKIAKQTMNYIALVGCCLPFPTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NSGVSCELEINLYKIAKQTMNYIALVGCCLPFPTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTITITIIIFLFCFLPYHTLRVHLTTWKVGLCKDRLHKALVITTLAANAACF 300
DB 241 SHRKALTTITITIIIFLFCFLPYHTLRVHLTTWKVGLCKDRLHKALVITTLAANAACF 300
QY 301 NPLLYFAGENFKDRLKSALRKQHPQAKTKCVFPVSVWLKRETRV 346
DB 301 NPLLYFAGENFKDRLKSALRKQHPQAKTKCVFPVSVWLKRETRV 346

RESULT 12
US-10-131-332A-2
Sequence 2, Application US/10131332A
Publication No. US2003020383A1
GENERAL INFORMATION:
APPLICANT: Ignar, Diane
TITLE OF INVENTION: Cyteine leukotriene 2 Receptor Polymorphism and Asthma
FILE REFERENCE: PU4824
CURRENT APPLICATION NUMBER: US/10/131,332A
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-332A-2

Query Match 100.0%; Score 1788; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKMSLOPSTISVSSEMEPNGTFSNNNSRNCCTIENKREFFPIVYLIIFPWGVLGNGLSI 60
DB 1 MERKMSLOPSTISVSSEMEPNGTFSNNNSRNCCTIENKREFFPIVYLIIFPWGVLGNGLSI 60
QY 61 YVFLQPYKKSSTSVNVMNLAIISDLFLSTLPFRADYLRGSNWIIFGDLACRIMSYSLYV 120
DB 61 YVFLQPYKKSSTSVNVMNLAIISDLFLSTLPFRADYLRGSNWIIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTISRANILCGIILWILIMASSIMLDGSGSQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTISRANILCGIILWILIMASSIMLDGSGSQ 180
QY 181 NSGVSCELEINLYKIAKQTMNYIALVGCCLPFPTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NSGVSCELEINLYKIAKQTMNYIALVGCCLPFPTLSICYLLIIRVLKVEVPESGLRV 240

QY 241 SHRKALTTITITIIIFLFCFLPYHTLRVHLTTWKVGLCKDRLHKALVITTLAANAACF 300
DB 241 SHRKALTTITITIIIFLFCFLPYHTLRVHLTTWKVGLCKDRLHKALVITTLAANAACF 300
QY 301 NPLLYFAGENFKDRLKSALRKQHPQAKTKCVFPVSVWLKRETRV 346
DB 301 NPLLYFAGENFKDRLKSALRKQHPQAKTKCVFPVSVWLKRETRV 346

RESULT 13
US-10-369-405-30
Sequence 30, Application US/10369405
Publication No. US20030224400A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMT11, AND VARIANTS
FILE REFERENCE: D0075A CIP
CURRENT APPLICATION NUMBER: US/10/369,405
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: U.S. 60/249,613
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: U.S. 09/991,225
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: U.S. 60/257,611
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: U.S. 60/305,818
PRIOR FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin version 3.2
SEQ ID NO 30
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-10-369-405-30

Query Match 100.0%; Score 1788; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKMSLOPSTISVSSEMEPNGTFSNNNSRNCCTIENKREFFPIVYLIIFPWGVLGNGLSI 60
DB 1 MERKMSLOPSTISVSSEMEPNGTFSNNNSRNCCTIENKREFFPIVYLIIFPWGVLGNGLSI 60
QY 61 YVFLQPYKKSSTSVNVMNLAIISDLFLSTLPFRADYLRGSNWIIFGDLACRIMSYSLYV 120
DB 61 YVFLQPYKKSSTSVNVMNLAIISDLFLSTLPFRADYLRGSNWIIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTISRANILCGIILWILIMASSIMLDGSGSQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTISRANILCGIILWILIMASSIMLDGSGSQ 180
QY 181 NSGVSCELEINLYKIAKQTMNYIALVGCCLPFPTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NSGVSCELEINLYKIAKQTMNYIALVGCCLPFPTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTITITIIIFLFCFLPYHTLRVHLTTWKVGLCKDRLHKALVITTLAANAACF 300
DB 241 SHRKALTTITITIIIFLFCFLPYHTLRVHLTTWKVGLCKDRLHKALVITTLAANAACF 300
QY 301 NPLLYFAGENFKDRLKSALRKQHPQAKTKCVFPVSVWLKRETRV 346
DB 301 NPLLYFAGENFKDRLKSALRKQHPQAKTKCVFPVSVWLKRETRV 346

RESULT 14
US-10-182-605-2
Sequence 2, Application US/10182605
Publication No. US20040023861A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: N78955A

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; CURRENT APPLICATION NUMBER: US/10/182,605
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0003079.1
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-605-2

Query Match          100.0%; Score 1788; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFMGVLGNGLSI 60
DB 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFMGVLGNGLSI 60
QY 61 YVFLQPYKSTSVNVFMLNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
DB 61 YVFLQPYKSTSVNVFMLNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIITWILMASSIMLDSGSEQ 180
DB 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIITWILMASSIMLDSGSEQ 180
QY 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLIIIRVLKVEVPEGSLRV 240
DB 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLIIIRVLKVEVPEGSLRV 240
QY 241 SHRKALTTIIITLIIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
DB 241 SHRKALTTIIITLIIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
QY 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFPVSWLKRKTRV 346
DB 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFPVSWLKRKTRV 346

RESULT 15
US-10-403-161-22
; Sequence 22, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173

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; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 22
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-22

Query Match          100.0%; Score 1788; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFMGVLGNGLSI 60
DB 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFFPIVYLIIFFMGVLGNGLSI 60
QY 61 YVFLQPYKSTSVNVFMLNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
DB 61 YVFLQPYKSTSVNVFMLNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIITWILMASSIMLDSGSEQ 180
DB 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIITWILMASSIMLDSGSEQ 180
QY 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLIIIRVLKVEVPEGSLRV 240
DB 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLIIIRVLKVEVPEGSLRV 240
QY 241 SHRKALTTIIITLIIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
DB 241 SHRKALTTIIITLIIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
QY 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFPVSWLKRKTRV 346
DB 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFPVSWLKRKTRV 346

Search completed: December 13, 2004, 18:05:05
Job time : 149 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:43:39 ; Search time 41 Seconds

(without alignments)
811.976 Million cell updates/sec

Title: US-09-980-049-1

Perfect score: 1788

Sequence: 1 MEKKMSLQPSISVSEMEPN.....KATKCVFVSVLKRRTY 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	26.3	362	2 S33733	G protein-coupled
2	447.5	25.0	370	2 JC5549	heptahelical p2ys-
3	447	25.0	308	2 I50241	G protein-coupled
4	446	24.9	373	2 JC4737	G protein-coupled
5	442	24.7	373	2 JC4162	p2y receptor - bov
6	440	24.6	361	2 B45680	G protein-coupled
7	436	24.4	344	2 T09508	intron 17 purinerg
8	421.5	23.6	373	2 A47556	ATP receptor P2u -
9	416	23.3	342	2 S13638	platelet-activatin
10	416	23.3	375	2 A54966	P-2U nucleotide re
11	409.5	22.9	342	2 A40191	platelet-activatin
12	406	22.7	420	2 I51667	thrombin receptor
13	404	22.6	341	2 S63666	platelet activatin
14	400.5	22.4	397	2 S66518	proteinase-activat
15	398	22.3	380	2 I38435	angiotensin recept
16	397	22.2	341	2 S43252	platelet-activatin
17	394.5	22.1	355	2 A45177	chemokine (C-C) re
18	394	22.0	359	2 I48705	proteinase activat
19	391	22.0	355	2 I49339	macrophage inflam
20	391	21.9	328	2 I55450	G protein-coupled
21	387	21.6	371	2 JC5796	probable chemotatr
22	382	21.4	371	2 JC5498	G protein-coupled
23	378.5	21.2	378	2 B55735	lymphocyte-specifi
24	378	21.1	355	2 JC5067	G protein-coupled
25	377.5	21.1	355	2 S68679	G protein-coupled
26	376	21.0	356	2 I49340	MIP-1 alpha recept
27	374.5	20.9	363	2 I57955	somatostatin recep
28	374.5	20.9	364	2 JN0763	somatostatin recep
29	374.5	20.9	383	2 S55594	G protein-coupled

30	373.5	20.9	387	2 I69202	G protein-coupled
31	372.5	20.8	378	2 A55735	G protein-coupled
32	372	20.8	363	2 I57940	somatostatin recep
33	371.5	20.8	365	2 S68208	G protein-coupled
34	367.5	20.6	427	2 S17148	alpha-thrombin rec
35	366.5	20.5	355	2 G02436	chemokine (C-C) re
36	366	20.5	352	2 JN0694	angiotensin II rec
37	363	20.3	359	2 S15403	angiotensin II rec
38	362.5	20.3	369	2 JC2083	somatostatin recep
39	361.5	20.2	352	2 A43113	chemokine (C-C) re
40	360	20.1	432	2 A43448	thrombin receptor
41	359	20.1	363	2 I48261	angiotensin II rec
42	357	20.0	328	2 JC4800	p2y6 receptor - hu
43	357	20.0	363	2 A49092	angiotensin II rec
44	356.5	19.9	333	2 I65989	G protein-coupled
45	356.5	19.9	361	2 JC5653	G protein-coupled

ALIGNMENTS

RESULT 1

S33733
G protein-coupled receptor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 06-Jan-1995 #sequence_rev1sion 06-Jan-1995 #ext_change 09-Jul-2004
C/Accession: S33733
R/Webb, T.E., Simon, J., Krisehek, B.J., Bateson, A.N., Smart, T.G., King, B.F., Burnsto
FEBS Lett. 324, 219-225, 1993
A/Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A/Reference number: S33733, PMID:93285340; PMID:8508924
A/Accession: S33733
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-362 <MEB>
A/Cross-references: UNIPROT:P34996; EMBL:X73268; NID:G395084; PIDN:CA51716.1; PID:G395
C/Superfamily: ATP receptor P2u
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.3%; Score 470; DB 2; Length 362;

Best local Similarity 30.6%; Pred. No. 6.1e-31;

Matches 99; Conservative 84; Mismatches 115; Indels 26; Gaps 7;

QY	16	EMEPNCTFSNNNSRNCCT--ENFKREFPIVYIIIFKGVGLNGLSIVFLQPKKSTSV 73	
DB	16	ELIAGCGAAGNATTKCSLTGTGFYLLPTVYLVITFGLNLSVAIMFVFHMRPWSGI 75	
QY	74	NVFMNLATSDILFISTLPFRADYLRGSMWTFGLACRIMSYSLVNMWSSIFLTYS 133	
DB	76	SVYMFNLADFLYVLTLPALIFTFYFNKTDWTFGDVWCKLQRTFHVNLIGSILFLCTS 135	
QY	134	VVFELAMVHPFRLIHTVTSIRSAWILGIIWILIMASSIML--DSGSBQNGSVTCLR- 189	
DB	136	VHRYTGVAHPKLSLGRKKKNAYVSSLVWALVANVIAPIPLFSGIVARNKTIIT- CYDT 194	
QY	190	-----LNTYKIAKLQTMNTIALVVGCLLPFTLSIYLLIIRVLLKVEYEPESGLRYSHRK 244	
DB	195	TADVYRSYFVSMCTTVMFCI-----PFIVILGCGYIIVKXLIYKLDNDSPLR--RK 246	
QY	245	ALTTIITLIIPLCLPYHTLTATVHL-----TTKVGICDGRKALKAVITTLAANA 298	
DB	247	SYLVITIVLVFVAVSYLPFVMTKLRLARLDQTPOMCAFNDKVATYATQVTRGLASNS 306	
QY	299	CENPLIYFAGENFKDRLKSLARK 322	
DB	307	CVDPIIYFLAGDFFRRRLSRATRK 330	

RESULT 2

JC5549
heptahelical p2ys-like receptor - human
C/Species: Homo sapiens (man)
C/Date: 02-Sep-1997 #sequence_rev1sion 05-Sep-1997 #ext_change 09-Jul-2004

Query Match **25.0%**; Score **447**; DB **2**; Length **308**;
Best Local Similarity **35.4%**; Pred. No. **3,9e-29**;
Matches **105**, Conservative **53**; Mismatches **119**; Indels **20**; Gaps **8**;

F.133-153/Domain: transmembrane #status predicted <TM>
F.177-201/Domain: transmembrane #status predicted <TM>
P.227-248/Domain: transmembrane #status predicted <TM6>
P.269-292/Domain: transmembrane #status predicted <TM7>

QY SRNCTIR-NFRARPEFFIVYLIFPMGVLGKGLSYVLPQPKYSTSVNPMLAISDLL 86
Db SSNCSTDSRKYTLTYGCVFSMVFVLGIANCVAIIYTFPLTKRNSETTMMALISDLL 62
QY FISTLPRADYYLRGNWFIIGDLACRIMSYSLLVMNYSSIFYPLTVLSVAFILAMVHPRL 146
Db FVTFLPFPRI-YYPFVRNWMPFGVDLYCKISVTLFTNMWGSLFLTGISDVRFLAIHVPFRS 121
QY LHTVSITSANILLGGIITIMLMASST---MLLDGSSEONGSVTSCLLENLYKIKLQTMY 203
Db KTTRIKENMARIVCAVAVITVALAGSTPASFPQSNTROQNNEQRCPFE-NPEESTWKTYLSR 180
QY IAA----VVGCLAPPFPLSLICYLLIIRLVLAVEPSGLARYSHRKALTITTIIPFLCF 260
Db IVETIEIVGFPIILNLNVOTSTWLRTLNK-PILTSENKSKKKVLMFVHLVIFCFC 239
QY 261 LPFY-----LTATVALTTMKVKGLCDRLHKALVITTLAANAACEPNLLDYYPAGE 310
Db 240 VPFVNI TLIVSWMT--QTWNCSVVTAIRTWYPTVLTCLAISNCEPDFIVYFTSD 293

RESULT 4

G protein-coupled receptor P2Y1 - human
Jc4737
N.Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C.Species: Homo sapiens (man)
C.Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C.Accession: Jc4737; Jc4615; S54253
R.Jamesons, R.; Communi, D.; Proctor, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A.Title: Cloning and tissue distribution of the human P2Y1 receptor.
A.Reference number: Jc4737; PMID:96205320; PMID:8630005
A.Accession: Jc4737
A.Molecule type: DNA
A.Residues: 1-373 <JAN>
R.Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Ahwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A>Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A.Reference number: Jc4615; PMID:96158962; PMID:8579591
A.Accession: Jc4615
A.Molecule type: mRNA
A.Residues: 1-373 <AYY>
A.Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A.Experimental source: erythro leukemia cells
R.Leon, C.; Vial, C.; Catzave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A.Description: Cloning of a human putative P2Y receptor.
A.Reference number: S54253
A.Accession: S54253
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-137,7-139-373 <LEO>
A.Cross-references: EMBL:I49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C.Comment: This receptor belongs to a family of G protein-coupled receptors. It responds
to Genetics:
A.Gene: p2y1; GDB:P2RY1
A.Cross-references: GDB:677125; OMIM:601167
A.Map position: 3pter-3qter
C.Superfamily: ATP receptor P2u
C.Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
#8-111/Domain: transmembrane #status predicted <TM>
F.124-152/Domain: transmembrane #status predicted <TM3>


```

Oy      304  LYYFAGENFEKDR LKSA LRKGHPQAKTKC 332
          :| :| :| :| :| :|
Db      292  IYCFELTKKFR--KHLTEKFYSMSSRKC 317

```

RESULT 12

151667
thrombin receptor - African clawed frog
C.Species: *Xenopus laevis* (African clawed frog)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Jul-2004
C.Accession: I51667
R.Gerstein, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Naneyicz, T.; Turck, C.W.; Vu, T.H.; Q
Nature 368, 648-651, 1994
A.Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
A.Reference number: I51667; PMID:4195429; PMID:8145852
A.Accession: I51667
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residue type: 1-420 <GB>
A.Cross-references: UniProt:P47749; EMBL:U09632; NID:G495197; PIDD:G4951

Query Match	22.7%;	Score 406;	DB 2;	Length 420;
Best Local Similarity	30.9%;	Pred. No. 1.2e-25;		
Matches 102;	Conservative 66;	Mismatches 128;	Indels 34;	Gaps 7;

[illegible]

RESULT 13

S63666
 platelet activating factor receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S63666
 C/Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
 Biochem. J. 314, 671-678, 1996
 A/Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization
 A/Reference number: S63666; MUID:96239129; PMID:8670084
 A/Accession: S63666
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-341 <ISH>
 A/Cross-References: UNIPROT:Q62035, EMBL:D50872, NID:g1255924, PIDN:BA09468.1, PID:g125
 A/Superfamily: ATP receptor P2u

```
Query Match      22.6%; Score 404; DB 2; Length 341;
Best Local Similarity 30.5%; Pred. No. 1.4e-25;
Matches 101; Conservative 66; Mismatches 134; Indels 30; Gaps 10;
```

[illegible]

RESULT 14

566518
proteinase-activated receptor 2 precursor - human
C|Species: Homo sapiens (man)
C|Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C|Accession: S66518; S64709; G02131
R|Nyseth, S.; Emlisson, K.; Larsson, A.K.; Strombeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A|Title: Molecular cloning and functional expression of the gene encoding the human prot
A|Reference number: S66518; MUID:96048032; PMID:7556175
A|Accession: S66518
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-397 <NVS->
A|CROSS-references: UNIPROT:P55085; EMBL:Z49993; NID:g1008084; PIDN:CA90290.1; PID:g100
R|Bohm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn
Biochem. J. 314, 1009-1016, 1996
A|Title: Molecular cloning, expression and potential functions of the human proteinase-a
A|Reference number: S64709; MUID:96177879; PMID:8615752
A|Accession: S64709
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-137, 'A', 139-397 <BOE>
A|CROSS-references: EMBL:U34038; NID:g1041728; PIDN:AA847871.1; PID:g1041729
R|Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A|Reference number: H00822

Query Match	22.4%	Score 400.5;	DB 2;	Length 397;
Best Local Similarity	30.7%;	Pred. No. 3.1e-25;		
Matches	99;	Conservative	69;	Mismatches 121;
			Indels	33;
			Gaps	9

```
Oy      40 FFFIVYLLIFFGVLGANGSLVIFQPKKSTSVNMFMNLASDLLFISTLPFRADYYL 99
        | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      77 FLPIVTITVVGVGLSPSGMALWFLPRKKHPRAVITMANIALDLSSVIMFKIATYHI 136
        | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy     100 RGSNMLFEDGLACRISYSLYNMSTSYFLTVLSVVFRLAMWHPRLIHVTSIRSNAILC 159
```

```
Db      137 HGNMWTIGBALCNVLIGFPFGNMTCSTLFTCTLSVQRWYIVNPMG-----HSRKKANIAI 192
Qy      160 GI---IWLIMASSIML-----LDGSEONGSVTSCLBLNLYKIAKLOTMYN-I 204
Db      193 GISLAIVLILVLTIPYVWQTIPIPAL-----NITTCNDVLPBQLVGMFNFL 244
Qy      205 ALVVGCLLPFTTISICYLIIIRVLKVEVPESGLRVSHRKALTTIIITLIIFLCPLPY 263
Db      245 SLAIGVFLFPAFLPASAYVIMIRLRSADENSEK-KRKRAIKLIYTVLAMYLICFTPS 303
Qy      264 HTLRTVHLTTWKVGLCDORLHKALVITLALAAANACFNPLLYFAGENFKDRLSKALRKG 323
Db      304 NLLLVHYFLIK-SQGSHYALYIVALCLSTLNSCIDPFYIVFVSHDFRDHAKNALL-- 360
Qy      324 HPQAKTKCVFPVSVWLKRETR 345
Db      361 -CRSVRTVKOMQVSLTSKHSR 381
```

RESULT 15

```
138435
angiotensin receptor homolog APJ - human
C:Species: Homo sapiens (man)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38435
R/O: Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
Gene 136, 355-360, 1993
A:Title: A human gene that shows identity with the gene encoding the angiotensin recep
A:Reference number: I38435; MUID:94124031; PMID:8294032
A:Accession: I38435
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <RES>
A:Cross-references: UNIPROT:P35414; EMBL:U03642; NID:G425351; PIDN:AAA18954.1; PID:G4253
A:Gene: APJ
A:Map position: 11q12
A:Intons: #status absent
C:Superfamily: vertebrate rhodopsin
```

```
Query Match      22.3% Score 398; DB 2; Length 380;
Best local Similarity 29.2%; Pred. No. 4.7e-25;
Matches 100; Conservative 71; Mismatches 134; Indels 38; Gaps 13;

Qy      17 MBPNGTFSN-----NNSRNCTIENFKRE--FFPIVYLIIFFWGVLGNGLSIY-VFLQPYKK 69
Db      1 MEEGDFDNYTGADNQECEYTDWKSSGALIPATYMLVFLGTTGNGLVMTVPRSSREK 60

Qy      70 STSVNVVMLMLAISDLLFITLPPRADYLRGSNWIFGDLACRIMSYSLYNNYSSIFYFL 129
Db      61 RRSADIFIASIAVADLTFVVTLLPLMATYTYRDYDWPFGTFCKLSYLIFFVNNYASVFC 120

Qy      130 TVLSVVRFLMVPFRLLHTSIRSANILGIIWL--IMASSIML-DGSEONGSVTS 166
Db      121 TGISFDRYLAIVRPVANARLRVSGAVAAVLAALAMPVAVLRTGDLNTYKQ 180

Qy      187 CLBLNLYKIAKLOT-----MNYIALVGCLEPFTLSICYLLIIRVL-----KVEV 233
Db      181 CY-MDYSMVATVSEMAWEVGLGVSTTVGFVVPFTIMLCYFPIAQTIAGHPRKERIE- 238

Qy      234 PEGGLRVSHRKALTTIIITLIIFPLCLPYHTLRTVH---LTTWKVGLCKDRILHKA 289
Db      239 ---GLR-KRRRLSLIYVAVLTFPALCWPMPYHLVKTLYMLGSLHWP---CDFDLFLMNIF 291

Qy      290 --TIALAANACFNPLLYFAGENFKDRLSKALRKGHPQAKT 330
Db      292 PYCTCISYVNSCLNPLIYAFDRFRQACTSMLCGGSRCAGT 334
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Search completed: December 13, 2004, 17:53:20
Job time : 42 secs

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